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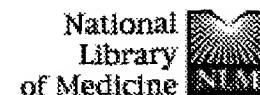
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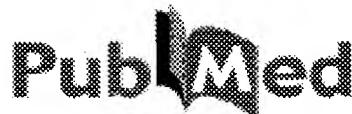
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TI The role of the ***hGRB14*** adaptor protein BPS domain in insulin
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AU Kelly, Sherrie Lynne [M.Sc.]; Triggs-Raine, Barbara [advisor]
CS The University of Manitoba (Canada) (0303)
SO Masters Abstracts International, (2003) Vol. 41, No. 5, p. 1378. order
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TI Human growth factor receptor bound 14 binds the activated insulin receptor and alters the insulin-stimulated tyrosine phosphorylation levels of multiple proteins.

AU Hemming, Richard; Agatep, Ronald; Badiani, Ketan; Wyant, Kerrie; Arthur, Gilbert; Gietz, R. Daniel; Triggs-Raine, Barbara [Reprint author]

CS Department of Biochemistry and Medical Genetics, University of Manitoba, 770 Bannatyne Avenue, Winnipeg, MB, R3E 0W3, Canada
traine@ms.umanitoba.ca

SO Biochemistry and Cell Biology, (2001) Vol. 79, No. 1, pp. 21-32. print.
CODEN: BCBIEQ. ISSN: 0829-8211.

DT Article

LA English

ED Entered STN: 14 Mar 2001
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AN 2001:38658 DISSABS Order Number: AAIMQ51679

TI The insulin signaling pathway: Evidence that Tax1bp1/Txbp151 is a dimeric human Grb14 interacting protein

AU Agatep, Ronald [M.Sc.]; Gietz, R. D. [adviser]

CS The University of Manitoba (Canada) (0303)

SO Masters Abstracts International, (2000) Vol. 39, No. 1, p. 151. Order No.: AAIMQ51679. 143 pages.

ISBN: 0-612-51679-2.

DT Dissertation

FS MAI

LA English

L2 ANSWER 4 OF 4 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN

AN 2000:576640 SCISEARCH

GA The Genuine Article (R) Number: 313NK

TI Effect of overexpression of ***hGrb14*** on Akt kinase and insulin signalling

AU Badiani K (Reprint); Hemming R; Gietz R D; TriggsRaine B

SO DIABETES, (MAY 2000) Vol. 49, Supp. [1], pp. 1359-1359.

Publisher: AMER DIABETES ASSOC, 1660 DUKE ST, ALEXANDRIA, VA 22314.
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DT Conference; Journal

FS LIFE; CLIN

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=> S Grb14 OR Grb10 OR Grb7

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L3 1778 GRB14 OR GRB10 OR GRB7

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 GA The Genuine Article (R) Number: 746XW
 TI Grb10 exceeding the boundaries of a common signaling adapter
 AU Riedel H (Reprint)
 CS Wayne State Univ, Dept Biol Sci, 2171 BSB, Detroit, MI 48202 USA
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 GA The Genuine Article (R) Number: 746XW
 TI Grb10: More than a simple adaptor protein
 AU Lim M A; Riedel H; Liu F (Reprint)
 CS Univ Texas, Hlth Sci Ctr, Dept Pharmacol, 7703 Floyd Curl Dr, San Antonio,
 TX 78229 USA (Reprint); Univ Texas, Hlth Sci Ctr, Dept Pharmacol, San
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 LA English
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 AN 2003:1051131 SCISEARCH
 GA The Genuine Article (R) Number: 746XW
 TI Grb7 in intracellular signaling and its role in cell regulation
 AU Shen T L; Guan J L (Reprint)
 CS Cornell Univ, Dept Mol Med, Ithaca, NY 14853 USA (Reprint)
 CYA USA
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 AN 2003:43622 DISSABS Order Number: AAI3075524
 TI Structural and functional analysis of the BPS and SH2 domains of Grb10
 AU Stein, Evan Gary [Ph.D.]; Hubbard, Stevan R. [advisor]
 CS New York University (0146)
 SO Dissertation Abstracts International, (2003) Vol. 63, No. 12B, p. 5687.
 Order No.: AAI3075524. 91 pages.
 ISBN: 0-493-95827-4.

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 AN 2003:59360 DISSABS Order Number: AAIMQ76780
 TI The role of the hGRB14 adaptor protein BPS domain in insulin signaling
 AU Kelly, Sherrie Lynne [M.Sc.]; Triggs-Raine, Barbara [advisor]
 CS The University of Manitoba (Canada) (0303)
 SO Masters Abstracts International, (2003) Vol. 41, No. 5, p. 1378. Order

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AN 2003:761870 CAPLUS
DN 139:287335
TI Gene expression profiling in the brain of rat models and use of nucleotide sequences as gene chips for screening antidepressants
IN Yoshikawa, Takeo; Nakaya, Noriaki; Aburaya, Hiroyuki
PA Institute of Physical and Chemical Research, Japan
SO Jpn. Kokai Tokkyo Koho, 18 pp.
CODEN: JKXXAF

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LA Japanese

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AN 10399185 IFIPAT;IFIUDB;IFICDB
TI DIAGNOSIS OF DISEASES ASSOCIATED WITH THE IMMUNE SYSTEM BY DETERMINING CYTOSINE METHYLATION
IN Berlin Kurt (DE); Olek Alexander (DE); Piepenbrock Christian (DE)
PA Unassigned Or Assigned To Individual (68000)
PI US 2003143606 A1 20030731
AI US 2002-311455 20021216
WO 2001-EP7537 20010702
20021216 PCT 371 date
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PRAI DE 2000-10032529 20000630
DE 2000-10043826 20000901
FI US 2003143606 20030731
DT Utility; Patent Application - First Publication
FS CHEMICAL
APPLICATION
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AN 10385219 IFIPAT;IFIUDB;IFICDB
TI GDU, A NOVEL SIGNALLING PROTEIN
IN Daly Roger John (AU); Sutherland Robert Lyndsay (AU)
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FI US 2003129639 20030710
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DT Utility; Patent Application - First Publication
FS CHEMICAL
APPLICATION
CLMN 9

GI 3 Figure(s).

FIG. 1 shows a schematic representation of ***Grb14*** structure with a restriction map for the ***Grb14*** cDNA and the cDNA clones used to derive the ***Grb14*** sequence aligned underneath. The initial clone isolated by CORT screening was designated clone 1. Two other clones (1-1 and 1-2) were isolated from the 184 cell line library by screening using clone 1 as a probe. The ***Grb14*** cDNA sequence was completed using two clones L5 and L6, isolated from a human liver cDNA library. Abbreviations are as follows: A; Apa I; Av; Avr II, X; Xho I; E; Eco RI. The numbers refer to distance in bp.

FIG. 2 shows the nucleotide and amino acid sequence of ***Grb14***. The PH domain is underlined and the SH2 domain indicated by bold type. The translation termination codon is shown by an asterisk in the amino acid sequence. Numbers refer to distances in bp.

FIG. 3 shows the sequence homology between ***Grb14***, Grb7, Grb10

and F10E9.6. As alignment of the amino acid sequences of ***Grb14***, mouse Grb7, mouse Grb10 and *C. elegans* F10E9.6 was obtained using the computer programs Clustal W and SeqVu. Identical residues are boxed. A highly conserved proline-rich motif is indicated by the dotted underline, the PH domain by the broken underline and the SH2 domain by the bold underline. Only the central region of F10E9.6 exhibiting homology with the Grb7 family is shown. Amino acid residues for each protein are numbered (from the initiation methionine) on the right.

L6 ANSWER 9 OF 135 IFIPAT COPYRIGHT 2004 IFI on STN DUPLICATE 4

AN 10360583 IFIPAT;IFIUDB;IFICDB

TI METHODS AND COMPOSITIONS FOR INHIBITING GRB7

IN Krag David N; oligino Lyn; Pero Stephanie C

PA Unassigned Or Assigned To Individual (68000)

PI US 2003105000 A1 20030605

AI US 2001-13815 20011105

PRAI US 2000-245755P 20001103 (Provisional)

FI US 2003105000 20030605

DT Utility; Patent Application - First Publication

FS CHEMICAL

APPLICATION

CLMN 93

GI 16 Figure(s).

FIG. 1 is a histogram showing the binding of Grb7 binding peptides (G7BP) to the SH2 domain of human Grb7 by ELISA.

FIG. 2 is a histogram showing the binding of a control phage clone to the SH2 domain of Grb2 but not to the SH2 domain of Grb7.

FIG. 3 is a histogram showing the effect of mutation on a G7BP-4 phage clone on its ability to bind to the SH2 domain of Grb7.

FIG. 4 is a histogram showing the binding specificity of seven Grb7 binding peptides to the SH2 domains of Grb7, Grb7 beta D5beta D6, ***Grb14***, full length Grb2, and BSA using a phage ELISA.

FIG. 5A is a graph showing the inhibition of G7-18 peptide-phage binding to Grb7-SH2 with the free synthetic peptides G7-18, G718NATE and G7-8.

FIG. 5B is a graph showing the inhibition of G7-8NA peptidephage binding to Grb7-SH2 with the free synthetic peptides G7-8, G7-8NA and G7-8NATE.

FIG. 6A is a graph showing G7-18NATE inhibits the association of Grb7 with the ErbB family of receptors, as detected by antiphosphotyrosine.

FIG. 6B is a densitometric analysis of autoradiographs using the Biorad Fluor-S Multimager with Quantity One 4.2.1 software, showing G7-18NATE inhibits the association of Grb7, not Grb2, with the ErbB family in a dose-dependent manner.

FIG. 7A is a graph showing that G7-18NATE inhibits the association of Grb7 with ErbB3 specifically in a dose-dependent manner, as detected by anti-ErbB3 FIG. 7B is a densitometric analysis of autoradiographs using the Biorad Fluor-S Multimager with Quantity One 4.2.1 software showing that G7-18NATE inhibits the association of Grb7 with ErbB3 in a dose-dependent manner.

FIG. 8A is a graph showing that G7-18NATE inhibits the association of Grb7 with ErbB2 specifically in a dose-dependent manner, as detected by anti-ErbB2.

FIG. 8B is a densitometric analysis of autoradiographs using the Biorad Fluor-S Multimager with Quantity One 4.2.1 software showing that G7-18NATE inhibits the association of Grb7 with ErbB2 in a dose-dependent manner.

FIG. 9A is one possible chemical structure for G7BP-4NATE (SEQ ID NO:50). Other thioether linkages are illustrated in FIGS. 9B, 9C, 9D and 9E, and it is to be understood that any of these linkages can be used in the formation of G7BP-4NATE.

FIG. 9B is the structure of a thioether containing peptide (G1TE) . This structure illustrates one possible thioether linkage between the N and C terminals of a peptide that can be used in the thioether containing peptides of the invention.

FIG. 9C is another possible structure for the thioether containing peptide GI TE. This structure illustrates one possible thioether linkage between the N and C terminals of a peptide that can be used in the thioether containing peptides of the invention.

FIG. 9D is another possible structure for the thioether containing peptide G1TE. This structure illustrates one possible thioether linkage between the N and C terminals of a peptide that can be used in the thioether containing peptides of the invention.

FIG. 9E is another possible structure for the thioether containing peptide GI TE. This structure illustrates one possible thioether linkage between the N and C terminals of a peptide that can be used in the thioether containing peptides of the invention.

L6 ANSWER 10 OF 135 IFIPAT COPYRIGHT 2004 IFI on STN DUPLICATE 5
 AN 10300425 IFIPAT;IFIUDB;IFICDB
 TI GDU, A NOVEL SIGNALLING PROTEIN
 IN Daly Roger John (AU); Sutherland Robert Lyndsay (AU)
 PA Unassigned or Assigned To Individual (68000)
 PI US 2003044834 A1 20030306
 AI US 2002-242332 20020911
 RLI WO 1996-AU258 19960502 Section 371 PCT Filing UNKNOWN
 US 1998-945771 19980422 DIVISION 6465623
 PRAI AU 1995-2742 19950502
 FI US 2003044834 20030306
 US 6465623
 DT Utility; Patent Application - First Publication
 FS CHEMICAL
 APPLICATION
 CLMN 9
 GI 3 Figure(s).

FIG. 1 shows a schematic representation of ***Grb14*** structure with a restriction map for the ***Grb14*** cDNA and the cDNA clones used to derive the ***Grb14*** sequence aligned underneath. The initial clone isolated by CORT screening was designated clone 1. Two other clones (1-1 and 1-2) were isolated from the 184 cell line library by screening using clone 1 as a probe. The ***Grb14*** cDNA sequence was completed using two clones L5 and L6, isolated from a human liver cDNA library. Abbreviations are as follows: A; Apa I; AV; Avr II, X; Xho I; E; Eco RI. The numbers refer to distance in bp.

FIG. 2 shows the nucleotide and amino acid sequence of ***Grb14***. The PH domain is underlined and the SH2 domain indicated by bold type. The translation termination codon is shown by an asterisk in the amino acid sequence. Numbers refer to distances in bp.

FIG. 3 shows the sequence homology between ***Grb14***, Grb7, Grb10 and F10E9.6. As alignment of the amino acid sequences of ***Grb14***, mouse Grb7, mouse Grb10 and C. elegans F10E9.6 was obtained using the computer programs Clustal W and SeqVu. Identical residues are boxed. A highly conserved proline-rich motif is indicated by the dotted underline, the PH domain by the broken underline and the SH2 domain by the bold underline. Only the central region of F10E9.6 exhibiting homology with the Grb7 family is shown. Amino acid residues for each protein are numbered (from the initiation methionine) on the right.

L6 ANSWER 11 OF 135 USPATFULL on STN
 AN 2003:330145 USPATFULL
 TI Skin cell biomarkers and methods for identifying biomarkers using nucleic acid microarrays
 IN Dooley, Thomas P., Vestavia Hills, AL, UNITED STATES
 Curto, Ernest V., Huntsville, AL, UNITED STATES
 Davis, Richard L., JR., Homewood, AL, UNITED STATES
 PI US 2003232356 A1 20031218
 AI US 2003-361006 A1 20030210 (10)
 PRAI US 2002-354519P 20020208 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 1897
 INCL INCLM: 435/006.000
 INCLS: 702/020.000
 NCL NCLM: 435/006.000
 NCLS: 702/020.000
 IC [7]
 ICM: C12Q001-68
 ICS: G06F019-00; G01N033-48; G01N033-50

L6 ANSWER 12 OF 135 USPATFULL on STN
 AN 2003:225702 USPATFULL
 TI Polynucleotide encoding a novel pleckstrin homology domain and proline rich domain containing adapter protein, PMN29
 IN Finger, Joshua N., San Marcos, CA, UNITED STATES
 Perez-Villar, Juan J., Mercerville, NJ, UNITED STATES
 Rajashekhar, Reddy, Langhorne, PA, UNITED STATES
 Yang, Guchen, Morrisville, PA, UNITED STATES
 Kiener, Peter A., Doylestown, PA, UNITED STATES
 PI US 2003157514 A1 20030821
 AI US 2002-234816 A1 20020904 (10)
 PRAI US 2001-317063P 20010904 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 13865

INCL INCLM: 435/006.000
INCLS: 435/069.100; 435/320.100; 435/325.000; 530/350.000; 536/023.500;
435/007.200
NCL NCLM: 435/006.000
NCLS: 435/069.100; 435/320.100; 435/325.000; 530/350.000; 536/023.500;
435/007.200
IC [7]
ICM: C12Q001-68
ICS: G01N033-53; G01N033-567; C07H021-04; C12P021-02; C12N005-06;
C07K014-47
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 13 OF 135 USPATFULL on STN
AN 2003:37578 USPATFULL
TI Specimen-linked G protein coupled receptor database
IN Muraca, Patrick J., Pittsfield, MA, UNITED STATES
PI US 2003027223 A1 20030206
AI US 2002-184694 A1 20020628 (10)
PRAI US 2001-302316P 20010629 (60)
DT Utility
FS APPLICATION
LN.CNT 3618
INCL INCLM: 435/007.210
INCLS: 702/019.000
NCL NCLM: 435/007.210
NCLS: 702/019.000
IC [7]
ICM: G01N033-567
ICS: G06F019-00; G01N033-48; G01N033-50
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 14 OF 135 USPATFULL on STN
AN 2003:222015 USPATFULL
TI Compositions for the detection of blood cell and immunological response
gene expression
IN Cocks, Benjamin G., Sunnyvale, CA, United States
Stuart, Susan G., Montara, CA, United States
Seilhamer, Jeffrey J., Los Altos Hills, CA, United States
PA Incyte Corporation, Palo Alto, CA, United States (U.S. corporation)
PI US 6607879 B1 20030819
AI US 1998-23655 19980209 (9)
DT Utility
FS GRANTED
LN.CNT 3719
INCL INCLM: 435/006.000
INCLS: 435/069.100; 536/023.100; 536/024.100; 536/024.300; 536/024.310;
536/024.320; 536/024.330
NCL NCLM: 435/006.000
NCLS: 435/069.100; 536/023.100; 536/024.100; 536/024.300; 536/024.310;
536/024.320; 536/024.330
IC [7]
ICM: C12Q001-68
ICS: C07H021-00
EXF 435/6; 435/69.1; 536/22.1; 536/23.1; 536/24.1; 536/24.3-24.33
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 15 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 6
AN 2003:254017 BIOSIS
DN PREV200300254017
TI Structural basis for dimerization of the Grb10 src homology 2 domain.
Implications for ligand specificity.
AU Stein, Evan G.; Ghirlando, Rodolfo; Hubbard, Stevan R. [Reprint Author]
CS Skirball Institute of Biomolecular Medicine, New York University School of
Medicine, 540 First Ave., New York, NY, 10016, USA
hubbard@saturn.med.nyu.edu
SO Journal of Biological Chemistry, (April 11, 2003) vol. 278, No. 15, pp.
13257-13264. print.
CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
LA English
ED Entered STN: 28 May 2003
Last Updated on STN: 28 May 2003
L6 ANSWER 16 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 7

AN 2003:355616 BIOSIS
DN PREV200300355616
TI NIK is a component of the EGF/hereregulin receptor signaling complexes.
AU Chen, Danying; Xu, Liang-Guo; Chen, Lei; Li, Lixia; Zhai, Zhonghe; Shu, Hong-Bing [Reprint Author]
CS Department of Immunology, National Jewish Medical and Research Center, University of Colorado Health Sciences Center, 1400 Jackson Street, K516c, Denver, CO, 80206, USA
shuh@njc.org
SO Oncogene, (10 July, 2003) vol. 22, No. 28, pp. 4348-4355. print.
ISSN: 0950-9232 (ISSN print).
DT Article
LA English
ED Entered STN: 6 Aug 2003
Last Updated on STN: 6 Aug 2003

L6 ANSWER 17 OF 135 LIFESCI COPYRIGHT 2004 CSA on STN
AN 2003:53872 LIFESCI
TI The Grb10/Nedd4 Complex Regulates Ligand-Induced Ubiquitination and Stability of the Insulin-Like Growth Factor I Receptor
AU Vecchione, A.; Marchese, A.; Henry, P.; Rotin, D.; Morrione, A.*
CS Department of Urology and Kimmel Cancer Center, Thomas Jefferson University, BLSB Room 631, 233 South 10th St., Philadelphia, PA 19107; E-mail: Andrea.Morrione@mail.tju.edu
SO Molecular and Cellular Biology [Mol. Cell. Biol.], (20030500) vol. 23, no. 9, pp. 3363-3372.
ISSN: 0270-7306.
DT Journal
FS G
LA English
SL English

L6 ANSWER 18 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2003:476188 BIOSIS
DN PREV200300476188
TI Characterization of a novel gene (HGP1) potentially involved in osteosarcoma progression.
AU Eppert, Kolja [Reprint Author]; Aneliunas, Vicky [Reprint Author]; Wunder, Jay S. [Reprint Author]; Andrulis, Irene L. [Reprint Author]
CS Fred A. Litwin Centre for Cancer Genetics, Samuel Lunenfeld Research Institute, Mount Sinai Hospital, Toronto, ON, Canada
SO Proceedings of the American Association for Cancer Research Annual Meeting, (July 2003) Vol. 44, pp. 1041-1042. print.
Meeting Info.: 94th Annual Meeting of the American Association for Cancer Research. Washington, DC, USA. July 11-14, 2003.
ISSN: 0197-016X.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 15 Oct 2003
Last Updated on STN: 15 Oct 2003

L6 ANSWER 19 OF 135 BIOTECHNO COPYRIGHT 2004 Elsevier Science B.V. on STN
DUPLICATE
AN 2003:37386423 BIOTECHNO
TI Using gene expression profiling to identify the molecular basis of the synergistic actions of hepatocyte growth factor and vascular endothelial growth factor in human endothelial cells
AU Gerritsen M.E.; Tomlinson J.E.; Zlot C.; Ziman M.; Hwang S.
CS M.E. Gerritsen, 541 Parrott Drive, San Mateo, CA 94402, United States.
E-mail: meg570@comcast.net
SO British Journal of Pharmacology, (2003), 140/4 (595-610), 52 reference(s)
CODEN: BJPCBM ISSN: 0007-1188
DT Journal; Conference Article
CY United Kingdom
LA English
SL English

L6 ANSWER 20 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 9
AN 2003:451765 BIOSIS
DN PREV200300451765
TI Carcinogen mediated initiation of glial progenitors in the rat brain results in marked dependency of proliferation and differentiation by insulin and FGF-2.
AU Kokkinakis, Demetrius Michael [Reprint Author]; Yang, Shuting [Reprint

Author]
CS University of Pittsburgh, Pittsburgh, PA, USA
SO Proceedings of the American Association for Cancer Research Annual
Meeting, (July 2003) Vol. 44, pp. 482. print.
Meeting Info.: 94th Annual Meeting of the American Association for Cancer
Research. Washington, DC, USA. July 11-14, 2003.
ISSN: 0197-016X.

DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)

LA English

ED Entered STN: 1 Oct 2003
Last Updated on STN: 1 Oct 2003

L6 ANSWER 21 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 10

AN 2003:587917 BIOSIS
DN PREV200300570714

TI The PIR domain of ***Grb14*** is an intrinsically unstructured
protein: Implication in insulin signaling.

AU Moncoq, Karine; Broutin, Isabelle [Reprint Author]; Larue, Valery;
Perdereau, Dominique; Cailliau, Katia; Browaeys-Poly, Edith; Burnol,
Anne-Francoise; Ducruix, Arnaud

CS Laboratoire de Cristallographie et RMN Biologiques, Faculte de Pharmacie
Paris 5, 4 avenue de l'Observatoire, 75270, Paris Cedex, 06, France
broutin@pharmacie.univ-paris5.fr

SO FEBS Letters, (20 November 2003) Vol. 554, No. 3, pp. 240-246. print.
CODEN: FEBLAS. ISSN: 0014-5793.

DT Article

LA English

ED Entered STN: 10 Dec 2003
Last Updated on STN: 10 Dec 2003

L6 ANSWER 22 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 11

AN 2003:390017 BIOSIS
DN PREV200300390017

TI Inhibition of FGF receptor signalling in Xenopus oocytes: Differential
effect of Grb7, Grb10 and ***Grb14***.

AU Cailliau, Katia; Le Marcis, Veronique; Bereziat, Veronique; Perdereau,
Dominique; Cariou, Bertrand; Vilain, Jean Pierre; Burnol, Anne-Francoise;
Browaeys-Poly, Edith [Reprint Author]

CS Laboratoire de Biologie du Developpement, Universite des Sciences;
Technologies de Lille, UPRES UA 1033, IFR 118, Batiment SN3, Villeneuve
d'Ascq Cedex, France
edith.browaeys@univ-lille1.fr

SO FEBS Letters, (31 July, 2003) Vol. 548, No. 1-3, pp. 43-48. print.
CODEN: FEBLAS. ISSN: 0014-5793.

DT Article

LA English

ED Entered STN: 27 Aug 2003
Last Updated on STN: 27 Aug 2003

L6 ANSWER 23 OF 135 IFIPAT COPYRIGHT 2004 IFI on STN DUPLICATE 12
AN 10142689 IFIPAT;IFIUDB;IFICDB

TI GDU, A NOVEL SIGNALLING PROTEIN; IT MAY PROVIDE A TARGET IN DISEASES OR
CONDITIONS IN WHICH PLATELET DERIVED GROWTH FACTOR RECEPTOR (PDGFR) PLAYS
A REGULATORY ROLE E.G. WOUND HEALING, FIBROTIC CONDITIONS,
ATHEROSCLEROSIS

IN DALY ROGER JOHN (AU); SUTHERLAND ROBERT LINDSAY (AU)

PA Unassigned Or Assigned To Individual (68000)

PPA Garvan Institute of Medical Research AU (Probable)

PI US 2002086328 A1 20020704

AI US 1998-945771 19980422

WO 1996-US258 19960502

FI US 2002086328 20020704
US 6465623 20021015

DT Utility; Patent Application - First Publication

FS CHEMICAL
APPLICATION

CLMN 9

GI 3 Figure(s).

FIG. 1 shows a schematic representation of ***Grb14*** structure with
a restriction map for the ***Grb14*** cDNA and the cDNA clones used
to derive the ***Grb14*** sequence aligned underneath. The initial
clone isolated by CORT screening was designated clone 1. Two other clones
(1-1 and 1-2) were isolated from the 184 cell line library by screening

using clone 1 as a probe. The ***Grb14*** cDNA sequence was completed using two clones L5 and L6, isolated from a human liver cDNA library. Abbreviations are as follows: A; Apa I; Av; Avr II, X; Xho I; E; Eco RI. The numbers refer to distance in bp.

FIG. 2 shows the nucleotide and amino acid sequence of ***Grb14***. The PH domain is underlined and the SH2 domain indicated by bold type. The translation termination codon is shown by an asterisk in the amino acid sequence. Numbers refer to distances in bp.

FIG. 3 shows the sequence homology between ***Grb14***, Grb7, Grb10 and F10E9.6. As alignment of the amino acid sequences of ***Grb14***, mouse Grb7, mouse Grb10 and C. elegans F10E9.6 was obtained using the computer programs Clustal W and SeqVu. Identical residues are boxed. A highly conserved proline-rich motif is indicated by the dotted underline, the PH domain by the broken underline and the SH2 domain by the bold underline. Only the central region of F10E9.6 exhibiting homology with the Grb7 family is shown. Amino acid residues for each protein are numbered (from the initiation methionine) on the right.

L6 ANSWER 24 OF 135 IFIPAT COPYRIGHT 2004 IFI on STN DUPLICATE 13
AN 10094016 IFIPAT;IFIUDB;IFICDB
TI POTENTIAL EFFECTOR FOR THE GRB7 FAMILY OF SIGNALLING PROTEINS; NUCLEOTIDE SEQUENCES CODING SIGNAL TRANSDUCTION PLYPEPTIDE; FOR USE IN THE DIAGNOSIS AND TREATMENT OF CANCERS
IN DALY ROGER JOHN (AU); SUTHERLAND ROBERT L (AU)
PA Unassigned Or Assigned To Individual (68000)
PI US 2002037582 A1 20020328
AI US 2000-509196 20000323
WO 1998-AU795 19980923
PRAI AU 1997-9388 19970923
FI US 2002037582 20020328
DT Utility; Patent Application - First Publication
FS CHEMICAL
CLMN APPLICATION
GI 15
2 Figure(s).

FIG. 1 provides the nucleotide and amino acid (single letter code) sequence of 2.2412. Numbers refer to distances in base pairs. Ankyrin-type repeat sequences are underlined. An additional repeat sequence is indicated by italics. The stop codon is represented by all asterisk. The original cDNA clone 2. 2412 isolated by the two hybrid screen spans nucleotides 6942664 of this sequence.

FIG. 2 provides a map of the 2.2412-binding region on ***Grb14***. A. Structure of the deletion constructs used in the analysis. Ga14 DNA-BD fusion constructs encoding full length ***Grb14*** (FL), the Nterminal (N), central region (C) and N-terminal+central region (N+C) were generated in the vector pAS2.1. B. Results of betagalactosidase activity assays following transformation of the above plasmids into yeast strain Y190 together with the original 2.2412 cDNA clone in PACT-2.

L6 ANSWER 25 OF 135 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:10730 CAPLUS
DN 136:49326
TI Diagnosis of diseases associated with the immune system using oligomer probes to detect cytosine methylation state
IN Olek, Alexander; Piepenbrock, Christian; Berlin, Kurt
PA Epigenomics A.-G., Germany
SO PCT Int. Appl., 32 pp.
CODEN: PIXXD2
DT Patent
LA German
FAN.CNT 68

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002000928	A2	20020103	WO 2001-EP7537	20010702
	WO 2002000928	A3	20020801		
	W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
	RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
	DE 10032529	A1	20020207	DE 2000-10032529	20000630
	EP 1274865	A2	20030115	EP 2001-953936	20010406

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
 IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
 JP 2003531589 T2 20031028 JP 2001-575634 20010406
 EP 1360319 A2 20031112 EP 2001-955278 20010406
 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
 IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
 EP 1294951 A2 20030326 EP 2001-967115 20010702
 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
 IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
 DE 20121966 U1 20031224 DE 2001-20121966 20010702
 US 2003143606 A1 20030731 US 2002-311455 20021216
 US 2003162194 A1 20030828 US 2003-240452 20030414
 PRAI DE 2000-10032529 A 20000630
 DE 2000-10043826 A 20000901
 DE 2000-10019058 A 20000406
 DE 2000-10019173 A 20000407
 WO 2001-EP3969 W 20010406
 WO 2001-EP4016 W 20010406
 EP 2001-967115 A 20010702
 WO 2001-EP7537 W 20010702

L6 ANSWER 26 OF 135 USPATFULL on STN
 AN 2002:315083 USPATFULL
 TI Nucleic acid sequences associated with baldness
 IN Pritchard, David, Seattle, WA, UNITED STATES
 Burmer, Glenna, Seattle, WA, UNITED STATES
 Brown, Joseph, Seattle, WA, UNITED STATES
 Demas, Vasiliki, Seattle, WA, UNITED STATES
 PI US 2002177566 A1 20021128
 AI US 2001-825096 A1 20010402 (9)
 PRAI US 2000-199745P 20000425 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 3768
 INCL INCLM: 514/044.000
 INCLS: 435/006.000; 435/007.210; 424/070.100
 NCL NCLM: 514/044.000
 NCLS: 435/006.000; 435/007.210; 424/070.100
 IC [7]
 ICM: A61K048-00
 ICS: C12Q001-68; G01N033-567; A61K007-06
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 27 OF 135 USPATFULL on STN
 AN 2002:181561 USPATFULL
 TI Process for in vitro selection of high methol producing genotypes
 IN Khanuja, Suman Preet Singh, Lucknow, INDIA
 Shasany, Ajit Kumar, Lucknow, INDIA
 Dhawan, Sunita, Lucknow, INDIA
 Darokar, Mahendra Pandurang, Lucknow, INDIA
 Kumar, Tiruppadiripuliyur Ranganathan Santha, Lucknow, INDIA
 Saikia, Dharmendra, Lucknow, INDIA
 Naqui, Arif Ali, Lucknow, INDIA
 Kumar, Sushil, Lucknow, INDIA
 PA Council of Scientific&Industrial Reaearch, New Delhi, INDIA (non-U.S.
 corporation)
 PI US 6423541 B1 20020723
 AI US 2000-531768 20000321 (9)
 DT Utility
 FS GRANTED
 LN.CNT 741
 INCL INCLM: 435/420.000
 INCLS: 435/410.000; 435/421.000; 435/430.000; 435/430.100; 435/431.000
 NCL NCLM: 435/420.000
 NCLS: 435/410.000; 435/421.000; 435/430.000; 435/430.100; 435/431.000
 IC [7]
 ICM: C12N005-00
 EXF 435/410; 435/420; 435/421; 435/430; 435/430.1; 435/431
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 28 OF 135 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
 AN 2002-547451 [58] WPIDS
 DNC C2002-155181
 TI Treatment or prophylaxis of a subject having a disorder characterized by
 abnormal interaction of Grb7 and a Grb7 ligand, involves administering to
 a non-phosphorylated peptide to a subject in need of the treatment.

DC B04 D16
IN Krag, D N; OLIBINO, L; PERO, S C
PA (UYVE-N) UNIV VERMONT & STATE AGRIC COLLEGE; (Krag-I) Krag D N; (OLIG-I)
OLIBINO L; (PERO-I) PERO S C
CYC 23
PI WO 2002036142 A2 20020510 (200258)* EN 95p A61K038-00
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR
W: AU CA JP
AU 2002020265 A 20020515 (200258) A61K038-00
US 2003105000 A1 20030605 (200339) A61K038-17
ADT WO 2002036142 A2 WO 2001-US47400 20011105; AU 2002020265 A AU 2002-20265
20011105; US 2003105000 A1 Provisional US 2000-245755P 20001103, US
2001-13815 20011105
FDT AU 2002020265 A Based on WO 2002036142
PRAI US 2000-245755P 20001103; US 2001-13815 20011105
IC ICM A61K038-00; A61K038-17

L6 ANSWER 29 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 14
AN 2002:492206 BIOSIS
DN PREV200200492206
TI Association of Grb7 with phosphoinositides and its role in the regulation
of cell migration.
AU Shen, Tang-Long; Han, Dong Cho; Guan, Jun-Lin [Reprint author]
CS Department of Molecular Medicine, Cornell University, Ithaca, NY, 14853,
USA
jg19@cornell.edu
SO Journal of Biological Chemistry, (August 9, 2002) Vol. 277, No. 32, pp.
29069-29077. print.
CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
LA English
ED Entered STN: 18 Sep 2002
Last Updated on STN: 18 Sep 2002

L6 ANSWER 30 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 15
AN 2002:292126 BIOSIS
DN PREV200200292126
TI Identification of novel non-phosphorylated ligands, which bind selectively
to the SH2 domain of Grb7.
AU Pero, Stephanie C.; Olibino, Lyn; Daly, Roger J.; Soden, Amy L.; Liu,
Chen; Roller, Peter P.; Li, Peng; Krag, David N. [Reprint author]
CS Department of Surgery, University of Vermont School of Medicine, Given
Medical Building, Rm. E309, Burlington, VT, 05405, USA
David.Krag@uvm.edu
SO Journal of Biological Chemistry, (April 5, 2002) Vol. 277, No. 14, pp.
11918-11926. print.
CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
LA English
ED Entered STN: 15 May 2002
Last Updated on STN: 15 May 2002

L6 ANSWER 31 OF 135 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:875636 CAPLUS
DN 138:151170
TI Comparative analysis of mutation frequency of coding and non coding short
mononucleotide repeats in mismatch repair deficient colorectal cancers
AU Duval, Alex; Reperant, Maryline; Hamelin, Richard
CS INSERM U434, CEPH, Paris, Fr.
SO Oncogene (2002), 21(52), 8062-8066
CODEN: ONCNES; ISSN: 0950-9232
PB Nature Publishing Group
DT Journal
LA English

RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 32 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 16
AN 2002:529717 BIOSIS
DN PREV200200529717
TI The adapter protein ZIP binds ***Grb14*** and regulates its inhibitory
action on insulin signaling by recruiting protein kinase Czeta.
AU Cariou, Bertrand; Perdereau, Dominique; Cailliau, Katia; Browaeys-Poly,

CS Edith; Bereziat, Veronique; Vasseur-Cognet, Mireille; Girard, Jean; Burnol, Anne-Francoise [Reprint author]
Departement d'Endocrinologie, Institut Cochin, CNRS-INSERM-Universite Rene Descartes, 24 Rue du Faubourg Saint-Jacques, 75674, Paris, France
burnol@cochin.inserm.fr

SO Molecular and Cellular Biology, (October, 2002) vol. 22, No. 20, pp. 6959-6970. print.
CODEN: MCEBD4. ISSN: 0270-7306.

DT Article
LA English
ED Entered STN: 16 Oct 2002
Last Updated on STN: 16 Oct 2002

L6 ANSWER 33 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 17

AN 2002:207358 BIOSIS
DN PREV200200207358

TI Inhibition of insulin receptor catalytic activity by the molecular adapter ***Grb14***.

AU Bereziat, Veronique; Kasus-Jacobi, Anne; Perdereau, Dominique; Cariou, Bertrand; Girard, Jean; Burnol, Anne-Francoise [Reprint author]

CS Endocrinologie et Metabolisme, CNRS UPR 1524, Institut Cochin de Genetique Moleculaire, 24 rue du Faubourg Saint-Jacques, 75674, Paris Cedex, 14, France
burnol@cochin.inserm.fr

SO Journal of Biological Chemistry, (February 15, 2002) vol. 277, No. 7, pp. 4845-4852. print.
CODEN: JBCHA3. ISSN: 0021-9258.

DT Article
LA English
ED Entered STN: 20 Mar 2002
Last Updated on STN: 20 Mar 2002

L6 ANSWER 34 OF 135 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2003:3572 CAPLUS
DN 138:382650

TI Ontogeny and the possible function of a novel epidermal growth factor-like repeat domain-containing protein, NELL2, in the rat brain

AU Kim, Hyun; Ha, Chang Man; Choi, Jungil; Choi, Eun Jung; Jeon, Jongrye; Kim, Changmee; Park, Sang Kyu; Kang, Sang Soo; Kim, Kyungjin; Lee, Byung Ju

CS Department of Anatomy, Brain Korea 21 Biomedical Sciences, Korea University College of Medicine, Seoul, S. Korea

SO Journal of Neurochemistry (2002), 83(6), 1389-1400
CODEN: JONRA9; ISSN: 0022-3042

PB Blackwell Science Ltd.

DT Journal
LA English

RE.CNT 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 35 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2002:396091 BIOSIS
DN PREV200200396091

TI Gene expression profiling of endometrial carcinomas: Identification of molecular biomarkers.

AU Yap, Oi Wah Stephanie [Reprint author]; Zhu, Shirley [Reprint author]; van de Rijn, Matt [Reprint author]; Longacre, Teri [Reprint author]; Teng, Nelson [Reprint author]; Husain, Amreen [Reprint author]

CS Stanford University Medical Center, Stanford, CA, USA

SO Proceedings of the American Association for Cancer Research Annual Meeting, (March, 2002) vol. 43, pp. 746. print.
Meeting Info.: 93rd Annual Meeting of the American Association for Cancer Research. San Francisco, California, USA. April 06-10, 2002.
ISSN: 0197-016X.

DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)

LA English

ED Entered STN: 24 Jul 2002
Last Updated on STN: 24 Jul 2002

L6 ANSWER 36 OF 135 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
AN 2002:207936 SCISEARCH
GA The Genuine Article (R) Number: 524UV
TI Comparison of gene expression in old versus young rat hippocampus by cDNA array

AU Cho K S; Choi J G; Ha C M; Son Y J; Choi W S; Lee B J (Reprint)
CS Univ Ulsan, Dept Biol Sci, Ulsan 680749, South Korea (Reprint); Gyeongsang
Nat'l Univ, Coll Med, Dept Anat, Chinju 660280, South Korea
CYA South Korea
SO NEUROREPORT, (4 MAR 2002) Vol. 13, No. 3, pp. 285-289.
Publisher: LIPPINCOTT WILLIAMS & WILKINS, 530 WALNUT ST, PHILADELPHIA, PA
19106-3621 USA.
ISSN: 0959-4965.
DT Article; Journal
LA English
REC Reference Count: 26
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L6 ANSWER 37 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 18
AN 2003:124261 BIOSIS
DN PREV200300124261
TI Assignment of backbone 1H, 13C, and 15N resonances of the SH2 domain of
human ***Grb14***.
AU Scharf, Paul J.; Lyons, Barbara A. [Reprint Author]
CS Department of Biochemistry, College of Medicine, University of Vermont,
Burlington, VT, 05405, USA
blyons@zoo.uvm.edu
SO Journal of Biomolecular NMR, (November 2002) Vol. 24, No. 3, pp. 275-276.
print.
ISSN: 0925-2738 (ISSN print).
DT Article
LA English
ED Entered STN: 5 Mar 2003
Last Updated on STN: 5 Mar 2003

L6 ANSWER 38 OF 135 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
AN 2002:524711 SCISEARCH
GA The Genuine Article (R) Number: 557XP
TI The atypical PKC-Interacting protein ZIP binds ***Grb14*** and
potentiates its inhibitory action on insulin signaling
AU Cariou B (Reprint); Perdereau D; Cailliau K; Browaeys-Poly E; Bereziat V;
Girard J; Burnol A F
SO DIABETES, (JUN 2002) Vol. 51, Supp. [2], pp. A56-A56. MA 228.
Publisher: AMER DIABETES ASSOC, 1660 DUKE ST, ALEXANDRIA, VA 22314 USA.
ISSN: 0012-1797.
DT Conference; Journal
LA English
REC Reference Count: 0

L6 ANSWER 39 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2003:155451 BIOSIS
DN PREV200300155451
TI Proteomic Study on the Retinas of RD, RDS and C3B Mice as Well as
Reconfirming of the Differentially Expressed Proteins by Using RT-PCT.
AU Li, D. [Reprint Author]; Zhang, Q. J.
CS Ocular Genetics and Molec Bio, Zhonghsan Ophthalmic Ctr, GuanZhou, China
SO ARVO Annual Meeting Abstract Search and Program Planner, (2002) Vol. 2002,
pp. Abstract No. 3629. cd-rom.
Meeting Info.: Annual Meeting of the Association For Research in Vision
and Ophthalmology. Fort Lauderdale, Florida, USA. May 05-10, 2002.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 26 Mar 2003
Last Updated on STN: 26 Mar 2003

L6 ANSWER 40 OF 135 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:798473 CAPLUS
DN 135:340282
TI Nucleic acid sequences associated with baldness and uses in detecting the
likelihood of baldness and for gene therapy
IN Pritchard, David; Burmer, Glenna; Brown, Joseph; Demas, Vasiliki
PA Lifespan Biosciences, Inc., USA
SO PCT Int. Appl., 87 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI WO 2001081628 A1 20011101 WO 2001-US12184 20010413
WO 2001081628 C2 20021227
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM,
HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS,
LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO,
RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ,
VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
US 2002177566 A1 20021128 US 2001-825096 20010402
PRAI US 2000-199745P P 20000425
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 41 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 19
AN 2001:390236 BIOSIS
DN PREV200100390236
TI Identification of a novel human tankyrase through its interaction with the
adaptor protein ***Grb14***.
AU Lyons, Ruth J.; Deane, Roisin; Lynch, Danielle K.; Ye, Zheng-Sheng
Jeffrey; Sanderson, Georgina M.; Eyre, Helen J.; Sutherland, Grant R.;
Daly, Roger J. [Reprint author]
CS Cancer Research Program, Garvan Institute of Medical Research, St.
Vincent's Hospital, Sydney, NSW, 2010, Australia
r.daly@garvan.org.au
SO Journal of Biological Chemistry, (May 18, 2001) Vol. 276, No. 20, pp.
17172-17180. print.
CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
LA English
OS Genbank-AF329696
ED Entered STN: 15 Aug 2001
Last Updated on STN: 23 Feb 2002

L6 ANSWER 42 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 20
AN 2001:514026 BIOSIS
DN PREV200100514026
TI The Grb7 family proteins: Structure, interactions with other signaling
molecules and potential cellular functions.
AU Han, Dong Cho; Shen, Tang-Long; Guan, Jun-Lin [Reprint author]
CS Cancer Biology Laboratories, Department of Molecular Medicine, Cornell
University, Ithaca, NY, 14853, USA
jg19@cornell.edu
SO Oncogene, (1 October, 2001) Vol. 20, No. 44, pp. 6315-6321. print.
CODEN: ONCNES. ISSN: 0950-9232.
DT Article
LA General Review; (Literature Review)
ED Entered STN: 7 Nov 2001
Last Updated on STN: 23 Feb 2002

L6 ANSWER 43 OF 135 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:634713 CAPLUS
DN 135:342315
TI Extensive characterization of genetic alterations in a series of human
colorectal cancer cell lines
AU Gayet, Jacqueline; Zhou, Xiao-Ping; Duval, Alex; Rolland, Sandra; Hoang,
Jean-Marc; Cottu, Paul; Hamelin, Richard
CS INSERM U434 - CEPH, Paris, 75010, Fr.
SO Oncogene (2001), 20(36), 5025-5032
CODEN: ONCNES; ISSN: 0950-9232
PB Nature Publishing Group
DT Journal
LA English
RE.CNT 63 THERE ARE 63 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 44 OF 135 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 21
AN 2001:170169 CAPLUS
DN 135:270832
TI Evolution of instability at coding and non-coding repeat sequences in
human MSI-H colorectal cancers

AU Duval, Alex; Rolland, Sandra; Compoint, Aurore; Tubacher, Emmanuel;
Iacopetta, Barry; Thomas, Gilles; Hamelin, Richard

CS INSERM U434, CEPH, Paris, 75010, Fr.

SO Human Molecular Genetics (2001), 10(5), 513-518

CODEN: HMGE5; ISSN: 0964-6906

PB Oxford University Press

DT Journal

LA English

RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 45 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 22

AN 2001:209006 BIOSIS

DN PREV200100209006

TI The BPS domain of Grb10 inhibits the catalytic activity of the insulin and IGF1 receptors.

AU Stein, Evan G.; Gustafson, Thomas A.; Hubbard, Stevan R. [Reprint author]

CS Department of Pharmacology, Skirball Institute of Biomolecular Medicine, New York University School of Medicine, 540 First Avenue, New York, NY, 10016, USA

hubbard@tallis.med.nyu.edu

SO FEBS Letters, (30 March, 2001) Vol. 493, No. 2-3, pp. 106-111. print.

CODEN: FEBLAS. ISSN: 0014-5793.

DT Article

LA English

ED Entered STN: 2 May 2001

Last Updated on STN: 18 Feb 2002

L6 ANSWER 46 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

AN 2002:69396 BIOSIS

DN PREV200200069396

TI Inhibition of insulin receptors tyrosine kinase activity by the molecular adapter ***Grb14***.

AU Bereziat, V. [Reprint author]; Kasus-Jacobi, A. [Reprint author]; Perdereau, D. [Reprint author]; Girard, J. [Reprint author]; Burnol, A.-F. [Reprint author]

CS CNRS UPR1524, ICGM, 9 rue Jules Hetzel, 92190, Meudon, France

SO Biochemical Society Transactions, (2001) Vol. 29, No. 3, pp. A69. print.

Meeting Info.: 673rd Bristol Meeting of the Biochemical Society. Bristol, London, UK. April 10-12, 2000. Biochemical Society.

CODEN: BCSTB5. ISSN: 0300-5127.

DT Conference; (Meeting)

Conference; Abstract; (Meeting Abstract)

LA English

ED Entered STN: 16 Jan 2002

Last Updated on STN: 25 Feb 2002

L6 ANSWER 47 OF 135 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 23

AN 2001:131521 CAPLUS

DN 134:202914

TI Human growth factor receptor bound 14 binds the activated insulin receptor and alters the insulin-stimulated tyrosine phosphorylation levels of multiple proteins

AU Hemming, Richard; Agatep, Ronald; Badiani, Ketan; Wyant, Kerrie; Arthur, Gilbert; Gietz, R. Daniel; Triggs-Raine, Barbara

CS Department of Biochemistry & Medical Genetics, University of Manitoba, Winnipeg, MB, R3E 0W3, Can.

SO Biochemistry and Cell Biology (2001), 79(1), 21-32

CODEN: BCBIEQ; ISSN: 0829-8211

PB National Research Council of Canada

DT Journal

LA English

RE.CNT 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 48 OF 135 DISSABS COPYRIGHT (C) 2004 ProQuest Information and Learning Company; All Rights Reserved on STN

AN 2001:8470 DISSABS Order Number: AAINQ49934

TI Identification and characterization of downstream signaling partners of the endothelial cell-specific receptor tyrosine kinase, Tek/Tie-2

AU Jones, Nina [Ph.D.]; Dumont, Daniel J. [adviser]

CS University of Toronto (Canada) (0779)

SO Dissertation Abstracts International, (2000) Vol. 61, No. 6B, p. 2900.

Order No.: AAINQ49934. 175 pages.

ISBN: 0-612-49934-0.

DT Dissertation
FS DAI
LA English

L6 ANSWER 49 OF 135 DISSABS COPYRIGHT (C) 2004 ProQuest Information and Learning Company; All Rights Reserved on STN
AN 2001:38658 DISSABS Order Number: AAIMQ51679
TI The insulin signaling pathway: Evidence that Tax1bp1/Txbp151 is a dimeric human ***Grb14*** interacting protein
AU Agatep, Ronald [M.Sc.]; Gietz, R. D. [adviser]
CS The University of Manitoba (Canada) (0303)
SO Masters Abstracts International, (2000) Vol. 39, No. 1, p. 151. Order No.: AAIMQ51679. 143 pages.
ISBN: 0-612-51679-2.

DT Dissertation
FS MAI
LA English

L6 ANSWER 50 OF 135 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 24
AN 2000:666978 CAPLUS
DN 133:247252
TI ***Grb14*** proteins for screening compounds capable of modulating insulin receptor tyrosine kinase activity
IN Burnol, Anne-Francoise; Perdereau, Dominique; Kasus-Jacobi, Anne;
Bereziat, Veronique; Girard, Jean
PA Centre National De La Recherche Scientifique-CNRS, Fr.
SO PCT Int. Appl., 46 pp.
CODEN: PIXXD2

DT Patent
LA French

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000055634	A1	20000921	WO 2000-FR613	20000314
	W: AU, CA, JP, NZ, US, ZA RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	FR 2790956	A1	20000922	FR 1999-3159	19990315
	FR 2790956	B1	20030523		
	EP 1161687	A1	20011212	EP 2000-910938	20000314
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	NZ 514668	A	20030829	NZ 2000-514668	20000314
	ZA 2001007546	A	20020829	ZA 2001-7546	20010913
PRAI	FR 1999-3159	A	19990315		
	WO 2000-FR613	W	20000314		

RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 51 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 25
AN 2000:345087 BIOSIS
DN PREV200000345087
TI Association of fibroblast growth factor receptor 1 with the adaptor protein ***Grb14***. Characterization of a new receptor binding partner.
AU Reilly, John F.; Mickey, Gregory; Maher, Pamela A. [Reprint author]
CS Dept. of Cell Biology, The Scripps Research Institute, 10550 N. Torrey Pines Rd., CAL-3, La Jolla, CA, 92037, USA
SO Journal of Biological Chemistry, (March 17, 2000) Vol. 275, No. 11, pp. 7771-7778. print.
CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
LA English
ED Entered STN: 16 Aug 2000
Last Updated on STN: 7 Jan 2002

L6 ANSWER 52 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 26
AN 2000:224729 BIOSIS
DN PREV200000224729
TI Evidence for an interaction between the insulin receptor and Grb7. A role for two of its binding domains, PIR and SH2.
AU Kasus-Jacobi, Anne; Bereziat, Veronique; Perdereau, Dominique; Girard, Jean; Burnol, Anne-Francoise [Reprint author]
CS Endocrinologie Metabolisme et Developpement, CNRS, UPR 1524, 9 Rue Jules

SO Hetzel, 92190, Meudon, France
Oncogene, (April 13, 2000) Vol. 19, No. 16, pp. 2052-2059. print.
CODEN: ONCNES. ISSN: 0950-9232.
DT Article
LA English
ED Entered STN: 31 May 2000
Last Updated on STN: 5 Jan 2002

L6 ANSWER 53 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 27
AN 2000:334281 BIOSIS
DN PREV200000334281
TI Grb10 proteins in insulin-like growth factor and insulin receptor
signaling (Review).
AU Morrione, Andrea [Reprint author]
CS Kimmel Cancer Center, Thomas Jefferson University, 233 South 10th Street,
606 Bluemle Life Sciences Building, Philadelphia, PA, 19107-5541, USA
SO International Journal of Molecular Medicine, (Feb., 2000) Vol. 5, No. 2,
pp. 151-154. print.
ISSN: 1107-3756.
DT Article
LA English
ED Entered STN: 10 Aug 2000
Last Updated on STN: 7 Jan 2002

L6 ANSWER 54 OF 135 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:223032 CAPLUS
DN 130:247888
TI Potential effector protein for the Grb7 family of signaling proteins
IN Daly, Roger John; Sutherland, Robert Lyndsay
PA Garvan Institute of Medical Research, Australia
SO PCT Int. Appl., 26 pp.
CODEN: PIXXD2

DT Patent
LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9915647	A1	19990401	WO 1998-AU795	19980923
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	CA 2303760	AA	19990401	CA 1998-2303760	19980923
	AU 9892458	A1	19990412	AU 1998-92458	19980923
	AU 727305	B2	20001207		
	EP 1017802	A1	20000712	EP 1998-944896	19980923
	R: CH, DE, FR, GB, IT, LI, SE				
	JP 2001517435	T2	20011009	JP 2000-512939	19980923
	US 2002037582	A1	20020328	US 2000-509196	20000323
PRAI	AU 1997-9388	A	19970923		
	WO 1998-AU795	W	19980923		

RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 55 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 28
AN 2000:433637 BIOSIS
DN PREV200000433637
TI Identification of Tek/Tie2 binding partners. Binding to a multifunctional
docking site mediates cell survival and migration.
AU Jones, Nina; Master, Zubin; Jones, Jamie; Bouchard, Denis; Gunji, Yuji;
Sasaki, Hiroki; Daly, Roger; Alitalo, Kari; Dumont, Daniel J. [Reprint
author]
CS Sunnybrook and Women's College Health Sciences Centre, 2075 Bayview Ave.,
Research Bldg., S-227, Toronto, ON, M4N 3M5, Canada
SO Journal of Biological Chemistry, (Oct. 22, 1999) Vol. 274, No. 43, pp.
30896-30905. print.
CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
LA English

ED Entered STN: 11 Oct 2000
Last Updated on STN: 10 Jan 2002

L6 ANSWER 56 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 29

AN 1999:288188 BIOSIS
DN PREV199900288188

TI Sequence analysis identifies a Ras-associating (RA)-like domain in the N-termini of band 4.1/JEF domains and in the Grb7/10/14 adapter family.

AU Wojcik, Jerome; Girault, Jean-Antoine; Labesse, Gilles; Chomillier, Jacques; Mornon, Jean-Paul; Callebaut, Isabelle [Reprint author]

CS Systemes moleculaires et Biologie structurale, LMCP, CNRS UMR 7590, Universites Paris 6 et Paris 7, 4 place Jussieu, 75252, Paris Cedex 05, France

SO Biochemical and Biophysical Research Communications, (May 27, 1999) Vol. 259, No. 1, pp. 113-120. print.
CODEN: BBRCA9. ISSN: 0006-291X.

DT Article
LA English

ED Entered STN: 5 Aug 1999
Last Updated on STN: 5 Aug 1999

L6 ANSWER 57 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 30

AN 1998:491148 BIOSIS
DN PREV199800491148

TI Identification of the rat adapter ***Grb14*** as an inhibitor of insulin actions.

AU Kasus-Jacobi, Anne; Perdereau, Dominique; Auzan, Colette; Clouser, Eric; Van Obberghen, Emmanuel; Mauvais-Jarvis, Franck; Girard, Jean; Burnol, Anne-Francoise [Reprint author]

CS Endocrinologie Metabolisme et Developpement, CNRS, UPR 1524, 9 rue Jules Hetzel, 92190 Meudon, France

SO Journal of Biological Chemistry, (Oct. 2, 1998) Vol. 273, No. 40, pp. 26026-26035. print.
CODEN: JBCHA3. ISSN: 0021-9258.

DT Article
LA English
OS Genbank-AF076619

ED Entered STN: 18 Nov 1998
Last Updated on STN: 18 Nov 1998

L6 ANSWER 58 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 31

AN 1998:251777 BIOSIS
DN PREV199800251777

TI Interaction of the Grb10 adapter protein with the Raf1 and MEK1 kinases.

AU Nantel, Andre [Reprint author]; Mohammad-Ali, Khosro; Sherk, Jennifer; Posner, Barry I.; Thomas, David Y.

CS Eukaryotic Genet. Group, Biotechnol. Res. Inst., Natl. Res. Council, 6100 Royalmount, Montreal, PQ H4P 2R2, Canada

SO Journal of Biological Chemistry, (April 24, 1998) Vol. 273, No. 17, pp. 10475-10484. print.
CODEN: JBCHA3. ISSN: 0021-9258.

DT Article
LA English

ED Entered STN: 9 Jun 1998
Last Updated on STN: 12 Aug 1998

L6 ANSWER 59 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 32

AN 1998:225785 BIOSIS
DN PREV199800225785

TI Grb10 interacts differentially with the insulin receptor, insulin-like growth factor I receptor, and epidermal growth factor receptor via the Grb10 Src homology 2 (SH2) domain and a second novel domain located between the Pleckstrin homology and SH2 domains.

AU He, Weimin; Rose, David W.; Olefsky, Jerrold M.; Gustafson, Thomas A. [Reprint author]

CS Metabolex Inc., 3876 Bay Cent. Pl., Hayward, CA 94545, USA

SO Journal of Biological Chemistry, (March 20, 1998) Vol. 273, No. 12, pp. 6860-6867. print.
CODEN: JBCHA3. ISSN: 0021-9258.

DT Article
LA English

ED Entered STN: 20 May 1998

Last Updated on STN: 20 May 1998

L6 ANSWER 60 OF 135 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
AN 1998:907280 SCISEARCH
GA The Genuine Article (R) Number: 137GQ
TI A novel FGF signaling pathway u ***Grb14*** binds to FGF receptor 1.
AU Reilly J F (Reprint); Mickey G; Maher P A
CS SCRIPPS RES INST, DEPT CELL BIOL, LA JOLLA, CA 92037
CYA USA

SO MOLECULAR BIOLOGY OF THE CELL, (NOV 1998) Vol. 9, Supp. [S], pp. 1365-1365.
Publisher: AMER SOC CELL BIOLOGY, PUBL OFFICE, 9650 ROCKVILLE PIKE, BETHESDA, MD 20814.
ISSN: 1059-1524.

DT Conference; Journal
FS LIFE
LA English
REC Reference Count: 0

L6 ANSWER 61 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1998:443196 BIOSIS
DN PREV199800443196
TI The Grb7 family of signalling proteins.
AU Daly, Roger J. [Reprint author]
CS Cancer Res. Program, Garvan Inst. Med. Res., St. Vincent's Hosp., Sydney, NSW 2010, Australia
SO Cellular Signalling, (Oct., 1998) Vol. 10, No. 9, pp. 613-618. print.
CODEN: CESIEY. ISSN: 0898-6568.
DT Article
General Review; (Literature Review)
LA English
ED Entered STN: 21 Oct 1998
Last Updated on STN: 21 Oct 1998

L6 ANSWER 62 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1999:16001 BIOSIS
DN PREV199900016001
TI A novel FGF signaling pathway u ***GRB14*** binds to FGF receptor 1.
AU Reilly, John F.; Mickey, Gregory; Maher, Pamela A.
CS Dep. Cell Biol., Scripps Res. Inst., La Jolla, CA 92037, USA
SO Molecular Biology of the Cell, (Nov., 1998) Vol. 9, No. SUPPL., pp. 236A. print.
Meeting Info.: 38th Annual Meeting of the American Society for Cell Biology. San Francisco, California, USA. December 12-16, 1998. American Society for Cell Biology.
CODEN: MBCEEV. ISSN: 1059-1524.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 20 Jan 1999
Last Updated on STN: 20 Jan 1999

L6 ANSWER 63 OF 135 DISSABS COPYRIGHT (C) 2004 ProQuest Information and Learning Company; All Rights Reserved on STN
AN 97:70470 DISSABS Order Number: AAR0598267 (not available for sale by UMI)
TI ERBB RECEPTOR SIGNALLING IN HUMAN BREAST CANCER (TYROSINE KINASES)
AU JANES, PETER WARWICK [PH.D.]
CS UNIVERSITY OF NEW SOUTH WALES (AUSTRALIA) (0423)
SO Dissertation Abstracts International, (1997) Vol. 58, No. 6B, p. 2970.
Order No.: AAR0598267 (not available for sale by UMI).
DT Dissertation
FS DAI
LA English
ED Entered STN: 19971104
Last Updated on STN: 19971104

L6 ANSWER 64 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 33
AN 1998:28109 BIOSIS
DN PREV19980028109
TI Cloning, chromosome localization, expression, and characterization of an Src homology 2 and pleckstrin homology domain-containing insulin receptor binding protein hGrb10gamma.
AU Dong, Lily Q.; Du, Hongyan; Porter, Sarah G.; Kolakowski, Lee F., Jr.; Lee, Adrian V.; Mandarino, J.; Fan, Jianbing; Yee, Douglas; Liu, Feng

CS [Reprint author]
 Dep. Pharmacol., Univ. Texas Health Sci. Cent., 7703 Floyd Curl Dr., San Antonio, TX 78284-7764, USA

SO Journal of Biological Chemistry, (Nov. 14, 1997) vol. 272, No. 46, pp. 29104-29112. print.
 CODEN: JBCHA3. ISSN: 0021-9258.

DT Article
 LA English
 OS Genbank-AF001534
 ED Entered STN: 14 Jan 1998
 Last Updated on STN: 14 Jan 1998

L6 ANSWER 65 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 DUPLICATE 34

AN 1997:221295 BIOSIS
 DN PREV199799513011

TI Structural determinants of the interaction between the erbB2 receptor and the Src homology 2 domain of Grb7.

AU Janes, Peter W.; Lackmann, Martin; Church, W. Bret; Sanderson, Georgina M.; Sutherland, Robert L.; Daly, Roger J. [Reprint author]

CS Cancer Res. Program, Garvan Inst. Med. Res., St. Vincent's Hosp., Sydney, NSW 2010, Australia

SO Journal of Biological Chemistry, (1997) vol. 272, No. 13, pp. 8490-8497.
 CODEN: JBCHA3. ISSN: 0021-9258.

DT Article
 LA English
 ED Entered STN: 22 May 1997
 Last Updated on STN: 22 May 1997

L6 ANSWER 66 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 DUPLICATE 35

AN 1997:110178 BIOSIS
 DN PREV199799409381

TI Human GRB-IR-beta/GRB10: Splice variants of an insulin and growth factor receptor-binding protein with PH and SH2 domains.

AU Frantz, J. Daniel; Giorgetti-Peraldi, Sophie; Ottinger, Elizabeth A.; Shoelson, Steven E. [Reprint author]

CS Joslin Diabetes Cent., One Joslin Place, Boston, MA 02215, USA

SO Journal of Biological Chemistry, (1997) vol. 272, No. 5, pp. 2659-2667.
 CODEN: JBCHA3. ISSN: 0021-9258.

DT Article
 LA English
 ED Entered STN: 10 Mar 1997
 Last Updated on STN: 10 Mar 1997

L6 ANSWER 67 OF 135 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 36

AN 1997:26254 CAPLUS
 DN 126:43162

TI GDU: a new target for the erbB family of protein tyrosine kinases and a cDNA encoding it

IN Daly, Roger John; Sutherland, Robert Lyndsay
 PA Garvan Institute of Medical Research, Australia; Daly, Roger John; Sutherland, Robert Lyndsay
 SO PCT Int. Appl., 15 pp.
 CODEN: PIXXD2

DT Patent
 LA English
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9634951	A1	19961107	WO 1996-AU258	19960502
	W:	AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI			
	RW:	KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN			
	CA 2220016	AA	19961107	CA 1996-2220016	19960502
	AU 9654904	A1	19961121	AU 1996-54904	19960502
	AU 701733	B2	19990204		
	EP 840786	A1	19980513	EP 1996-911844	19960502
	R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI			
	JP 11505415	T2	19990521	JP 1996-532859	19960502
	US 2002086328	A1	20020704	US 1998-945771	19980422
	US 6465623	B2	20021015		

US 2003044834 A1 20030306 US 2002-242332 20020911
US 2003129639 A1 20030710 US 2002-323001 20021218
PRAI AU 1995-2742 A 19950502
WO 1996-AU258 W 19960502
US 1998-945771 A3 19980422
US 2002-242332 A3 20020911

L6 ANSWER 68 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 37
AN 1996:484539 BIOSIS
DN PREV199699199795
TI Cloning and characterization of ***GRB14***, a novel member of the
GRB7 gene family.
AU Daly, Roger J. [Reprint author]; Sanderson, Georgina M.; Janes, Peter W.;
Sutherland, Robert L.
CS Cancer Biol. Div., Garvan Inst. Med. Res., St. Vincent's Hosp., Sydney,
NSW 2010, Australia
SO Journal of Biological Chemistry, (1996) Vol. 271, No. 21, pp. 12502-12510.
CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
LA English
OS EMBL-L76687; Genbank-L76687
ED Entered STN: 24 Oct 1996
Last Updated on STN: 10 Dec 1996

L6 ANSWER 69 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 38
AN 1996:438181 BIOSIS
DN PREV199699151787
TI Assignment of the human ***GRB14*** gene to chromosome 2q22-q24 by
fluorescence in situ hybridization.
AU Baker, Elizabeth; Sutherland, Grant R.; Sutherland, Robert L.; Daly, Roger
J. [Reprint author]
CS Cancer Biol. Div., Garvan Inst. Med. Res., St. Vincent's Hosp., Sydney,
NSW 2010, Australia
SO Genomics, (1996) Vol. 36, No. 1, pp. 218-220.
CODEN: GNMCEP. ISSN: 0888-7543.
DT Article
LA English
OS EMBL-L76687; Genbank-L76687
ED Entered STN: 26 Sep 1996
Last Updated on STN: 5 Nov 1996

L6 ANSWER 70 OF 135 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
AN AAW07871 Protein DGENE
TI A new signalling protein designated GDU related to erbB receptor targets
- also DNA encoding it, probes, and monoclonal antibodies for detection
and treatment of breast and prostate cancer
IN Daly R J; Sutherland R L
PA (GARV-N) GARVAN INST MEDICAL RES.
PI WO 9634951 A1 19961107 17p
AI WO 1996-AU258 19960502
PRAI AU 1995-2742 19950502
DT Patent
LA English
OS 1996-506156 [50]
CR N-PSDB: AAT44581
DESC GDU (or ***Grb14***), a signalling protein.

L6 ANSWER 71 OF 135 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
AN AAX25366 cDNA DGENE
TI New candidate effector for the Grb7 family of signaling proteins, and
specific antibody, useful for detection and treatment of cancer
IN Daly R J; Sutherland R L
PA (GARV-N) GARVAN INST MEDICAL RES.
PI WO 9915647 A1 19990401 24p
AI WO 1998-AU795 19980923
PRAI AU 1997-9388 19970923
DT Patent
LA English
OS 1999-254707 [21]
CR P-PSDB: AAY05734
DESC Human Grb7 effector 2.2412 cDNA.

L6 ANSWER 72 OF 135 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
AN AAT44581 DNA DGENE

TI A new signalling protein designated GDU related to erbB receptor targets
 - also DNA encoding it, probes, and monoclonal antibodies for detection
 and treatment of breast and prostate cancer
 IN Daly R J; Sutherland R L
 PA (GARV-N) GARVAN INST MEDICAL RES.
 PI WO 9634951 A1 19961107 17p
 AI WO 1996-AU258 19960502
 PRAI AU 1995-2742 19950502
 DT Patent
 LA English
 OS 1996-506156 [50]
 CR P-PSDB: AAW07871
 DESC GDU (or ***Grb14***), a signalling protein.

L6 ANSWER 73 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AY419444 GenBank (R)
 GenBank ACC. NO. (GBN): AY419444
 GenBank VERSION (VER): AY419444.1 GI:39775401
 CAS REGISTRY NO. (RN): 629064-36-4
 SEQUENCE LENGTH (SQL): 1361
 MOLECULE TYPE (CI): DNA; linear
 DIVISION CODE (CI): Genome Survey Sequence
 DATE (DATE): 17 Dec 2003
 DEFINITION (DEF): Mus musculus ***GRB14*** gene, VIRTUAL TRANSCRIPT,
 partial sequence, genomic survey sequence.
 GSS
 KEYWORDS (ST):
 SOURCE: Mus musculus (house mouse)
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus

COMMENT:

These sequences were made by sequencing genomic exons and ordering them based on alignment.

REFERENCE:
 AUTHOR (AU): 1 (bases 1 to 1361)
 Clark,A.G.; Glanowski,S.; Nielson,R.; Thomas,P.;
 Kejariwal,A.; Todd,M.A.; Tanenbaum,D.M.; Civello,D.R.;
 Lu,F.; Murphy,B.; Ferriera,S.; Wang,G.; Zheng,X.H.;
 White,T.J.; Sninsky,J.J.; Adams,M.D.; Cargill,M.
 TITLE (TI): Inferring nonneutral evolution from human-chimp-mouse
 orthologous gene trios
 JOURNAL (SO): Science, 302 (5652), 1960-1963 (2003)
 REFERENCE:
 AUTHOR (AU): 2 (bases 1 to 1361)
 Clark,A.G.; Glanowski,S.; Nielson,R.; Thomas,P.;
 Kejariwal,A.; Todd,M.A.; Tanenbaum,D.M.; Civello,D.R.;
 Lu,F.; Murphy,B.; Ferriera,S.; Wang,G.; Zheng,X.H.;
 White,T.J.; Sninsky,J.J.; Adams,M.D.; Cargill,M.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (16-NOV-2003) Celera Genomics, 45 West Gude
 Drive, Rockville, MD 20850, USA

FEATURES (FEAT):	Feature Key	Location	Qualifier
source	1..1361	/organism="Mus musculus" /mol-type="genomic DNA" /db-xref="taxon:10090"	
gene	<1..>1361	/gene="GRB14" /locus-tag="HCM6892"	

SEQUENCE (SEQ):

1 atgagtctga gtgcaagaag agtcaccctg cctgcataa caccatagt tctacagaag
 61 aggnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
 121 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
 181 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn aaagaaccgt agaggaccac
 241 gagctgccaa ctgaagtgtc gtctcactgg ggagtggaaag aagacaataa gctgtatctt
 301 agaaaagaatt atgccaaata tgaattttt aagaacccaa tgnnnnnnnn nnnnnnnnnn
 361 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnngt
 421 ttttaagct ccagcacgta tcctgaaatc catggctct tacatgcaaa ggaacaggga
 481 aagaagtctt gaaaaaaagc ttactttttt ctcagaagat ctggcttata tttttctact
 541 aaaggcacat ccaaggaacc acggcatttg cagctttca gtgaattcag cactagtac
 601 gtttatatgt cactggcagg aaaaaaaaaa cacggagcgc caactcccta tggattctgc
 661 ttaaacctaa caaaggcagga gggccccggg acctgaaaat gctctgtgca gaagaagac
 721 agagcaggac gtgctgggtg accgccatcc gactgctgaa gnnnnnnnnn nnnnnnnnnn
 781 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn

841 nnagaagcgt atcagagaat tccctagtag caatggactt ctcaggtgag aagagcagag
 901 tcatagacaa ccccaactgaa gcgccttcgg ttgctgttga ggaaggcctc gcgtggagga
 961 aaaaaggctg tttacgcctg gggaaatcagc gaagccccag tgccccctcc cagagctctg
 1021 ctgtgaacat ggctctccat cggtcccaac catggttca ccacagaatt tccagagatg
 1081 aggctcagcg gctgatcatt cgccaggggc ctgtggatgg agttttcttgc ttagggata
 1141 gtcagagtaa ccccaagaact ttgttactgt caatgagtca tgacaaaag ataaaacact
 1201 atcaaattat acccgtagaa gatgtatggt agctgttcca tactctggat gatggccata
 1261 cgaagttcac agacctcatac cagctggggc agttctacca gctcaacagg ggggtcccttc
 1321 cttgcaagct gaagcattac tggcttagga tggctgttta g

L6 ANSWER 74 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AY419443 GenBank (R)
 GenBank ACC. NO. (GBN): AY419443
 GenBank VERSION (VER): AY419443.1 GI:39775400
 CAS REGISTRY NO. (RN): 629064-35-3
 SEQUENCE LENGTH (SQL): 1362
 MOLECULE TYPE (CI): DNA; linear
 DIVISION CODE (CI): Genome Survey Sequence
 DATE (DATE): 17 Dec 2003
 DEFINITION (DEF): *Pan troglodytes* ***GRB14*** gene, VIRTUAL
 TRANSCRIPT, partial sequence, genomic survey sequence.
 KEYWORDS (ST): GSS
 SOURCE: *Pan troglodytes* (chimpanzee)
 ORGANISM (ORGN): *Pan troglodytes*
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; *Pan*

COMMENT:

These sequences were made by sequencing genomic exons and ordering them based on alignment.

REFERENCE: 1 (bases 1 to 1362)
 AUTHOR (AU): Clark,A.G.; Glanowski,S.; Nielson,R.; Thomas,P.;
 Kejariwal,A.; Todd,M.A.; Tanenbaum,D.M.; Civello,D.R.;
 Lu,F.; Murphy,B.; Ferriera,S.; Wang,G.; Zheng,X.H.;
 White,T.J.; Sninsky,J.J.; Adams,M.D.; Cargill,M.
 TITLE (TI): Inferring nonneutral evolution from human-chimp-mouse
 orthologous gene trios
 JOURNAL (SO): Science, 302 (5652), 1960-1963 (2003)
 REFERENCE: 2 (bases 1 to 1362)
 AUTHOR (AU): Clark,A.G.; Glanowski,S.; Nielson,R.; Thomas,P.;
 Kejariwal,A.; Todd,M.A.; Tanenbaum,D.M.; Civello,D.R.;
 Lu,F.; Murphy,B.; Ferriera,S.; Wang,G.; Zheng,X.H.;
 White,T.J.; Sninsky,J.J.; Adams,M.D.; Cargill,M.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (16-NOV-2003) Celera Genomics, 45 West Gude
 Drive, Rockville, MD 20850, USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1362	/organism="Pan troglodytes" /mol-type="genomic DNA" /db-xref="taxon:9598"
gene	<1..>1362	/gene="GRB14" /locus-tag="HCM6892"

SEQUENCE (SEQ):

1 atgagtttga gtgcaagaag agtcactctg cctgcaataa cggcaataat tctacagaaa
 61 aggnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn
 121 nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn
 181 nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn
 241 gaactggta ttgaagtgtc atccaactgg gggatagaag aagaaaaacaa actannnnnn
 301 nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn
 361 nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn
 421 tttctgagtt caagcacata tcctgaaatt catggttct tacatgcgaa agaacaggaa
 481 aagaagtctt gaaaaaaat ttactttttt ctaagaagat ctggttata tttttctact
 541 aaaggaacat caaagnnnnn nnnnnnnnnnn nnnttttca gtgaatttgg caatagtgt
 601 atttatgtgt nnctggcagg caaaaaaaaaa catggagcac cgactannnn nnnnnnnnnnn
 661 nnnnnnccta acaaagcggg agggccccga gacctgaaaa tgctctgtgc agaagaagag
 721 cagacttagga cgtgctgggt gaccgcattt agattgttta agnnnnnnnnnn nnnnnnnnnnn
 781 nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn
 841 nnnagaagta tatcagagaa ttccctggta gcaatggaa tctcaggcca gaaaagcaga
 901 gttatagaaa atccnnntga agccctttca gttgcnnntg aagaaggact cgcttggagg
 961 nnnnnnnnnnn nnttacgnnt gggcaactcac ggtagccccca ctgcctcttc acagagctct
 1021 gccacaaaca tggctatcca ccggccccca ccatggtttc accacaaaat ttctagagat

1081 gaggctcagc gattgattat tcagcaagga cttgtggatg gnntttctt ggtacggat
 1141 agtcagagta accccaaaac ttcgtactg tcaatgagtc atggacaaaa aataaagcac
 1201 ttcaattttt taccagtaga agatgacggt gaaatgtcc acacactgga tcatggccac
 1261 acaagattta cagatcta atcagctgtg gagttctatc aactcaataa gggcggttctt
 1321 cttgcagaatg taaaacattt ttgtgcttagg attgctct ag

L6 ANSWER 75 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AY419442 GenBank (R)
 GenBank ACC. NO. (GBN): AY419442
 GenBank VERSION (VER): AY419442.1 GI:39775399
 CAS REGISTRY NO. (RN): 629064-34-2
 SEQUENCE LENGTH (SQL): 1362
 MOLECULE TYPE (CI): DNA; linear
 DIVISION CODE (CI): Genome Survey Sequence
 DATE (DATE): 17 Dec 2003
 DEFINITION (DEF): Homo sapiens ***GRB14*** gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
 KEYWORDS (ST): GSS
 SOURCE: Homo sapiens (human)
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo
 COMMENT:
 These sequences were made by sequencing genomic exons and ordering them based on alignment.
 REFERENCE:
 AUTHOR (AU): 1 (bases 1 to 1362)
 Clark,A.G.; Glanowski,S.; Nielson,R.; Thomas,P.;
 Kejariwal,A.; Todd,M.A.; Tanenbaum,D.M.; Civello,D.R.;
 Lu,F.; Murphy,B.; Ferriera,S.; Wang,G.; Zheng,X.H.;
 White,T.J.; Sninsky,J.J.; Adams,M.D.; Cargill,M.
 TITLE (TI): Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
 JOURNAL (SO): Science, 302 (5652), 1960-1963 (2003)
 REFERENCE:
 AUTHOR (AU): 2 (bases 1 to 1362)
 Clark,A.G.; Glanowski,S.; Nielson,R.; Thomas,P.;
 Kejariwal,A.; Todd,M.A.; Tanenbaum,D.M.; Civello,D.R.;
 Lu,F.; Murphy,B.; Ferriera,S.; Wang,G.; Zheng,X.H.;
 White,T.J.; Sninsky,J.J.; Adams,M.D.; Cargill,M.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1362	/organism="Homo sapiens" /mol-type="genomic DNA" /db-xref="taxon:9606"
gene	<1..>1362	/gene="GRB14" /locus-tag="HCM6892"

SEQUENCE (SEQ):

1 atgagtttga gtgcaagaag agtcactctg cctgcaataa cgccaataat tctacagaaa
 61 aggnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
 121 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
 181 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn aaagaacaat agaagaccac
 241 gaactggta ttgaagtgtc atccaaactgg gggatagaag aagaaaaacaa actataactt
 301 agaaaaaaatt atgccaaata ttagttctt aaaaacccaa tgnnnnnnnnn nnnnnnnnnn
 361 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnatg
 421 tttctgagtt caagcacata tcttggaaatt catggttct tacatgcgaa agaacaggaa
 481 aagaagtctt gaaaaaaat ttactttttt ctaagaagat ctggtttata tttttctact
 541 aaaggaacat caaagnaacc gccgcatttgc cttttttca gcaatgttgg caatagtgt
 601 atttatgtgt cactggcagg caaaaaaaaaa catggagcac cgactaacta tggattctgc
 661 ttaaggctt acaaagcggg agggccccga gacctgaaaaa tgcctctgtgc agaagaagag
 721 cagagtagga cttgtgggt gaccgcgatt agattgttta agnnnnnnnnn nnnnnnnnnn
 781 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
 841 nnnagaagta tatcagagaa ttccctggta gcaatggact tctcaggccca gaaaaggcaga
 901 gttatagaaa atcccactga agccctttca gttgcgggtt aagaaggact cgctggagg
 961 aaaaaaggat gtttacgcct gggcactcac ggtggccca ctgcctcttc acagagctct
 1021 gccacaaaaca tggctatcca ccggcccgag ccatggtttc accacaaaaat ttcttagagat
 1081 gaggtcagc gattgattat tcagcaagga cttgtggatg gagttttctt ggtacggat
 1141 agtcagagta accccaaaac tttcgtactg tcaatgagtc atggacaaaa aataaagcac
 1201 ttcaattttt taccagtaga agatgacggt gaaatgtcc acacactgga tcatggccac
 1261 acaagattta cagatcta atcagctgtg gagttctatc aactcaataa gggcggttctt

1321 ccttgcaagt tgaaacatta ttgtgctagg attgctctct ag

L6 ANSWER 76 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BC053559 GenBank (R)
GenBank ACC. NO. (GBN): BC053559
GenBank VERSION (VER): BC053559.1 GI:31657223
CAS REGISTRY NO. (RN): 535081-55-1
SEQUENCE LENGTH (SQL): 1872
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Primates
DATE (DATE): 12 Nov 2003
DEFINITION (DEF): Homo sapiens growth factor receptor-bound protein 14, mRNA (cDNA clone MGC:61485 IMAGE:6162863), complete cds.
KEYWORDS (ST): MGC
SOURCE: Homo sapiens (human)
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo

COMMENT:

Contact: MGC help desk
Email: cgapsbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nhgri.nih.gov

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghghi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 115 Row: m Column: 17

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4758477.

REFERENCE: 1 (bases 1 to 1872)

AUTHOR (AU): Strausberg,R.L.; Feingold,E.A.; Grouse,L.H.;
Derge,J.G.; Klausner,R.D.; Collins,F.S.; Wagner,L.;
Shenmen,C.M.; Schuler,G.D.; Altschul,S.F.; Zeeberg,B.;
Buetow,K.H.; Schaefer,C.F.; Bhat,N.K.; Hopkins,R.F.;
Jordan,H.; Moore,T.; Max,S.I.; Wang,J.; Hsieh,F.;
Diatchenko,L.; Marusina,K.; Farmer,A.A.; Rubin,G.M.;
Hong,L.; Stapleton,M.; Soares,M.B.; Bonaldo,M.F.;
Casavant,T.L.; Scheetz,T.E.; Brownstein,M.J.;
Usdin,T.B.; Toshiyuki,S.; Carninci,P.; Prange,C.;
Raha,S.S.; Loquellano,N.A.; Peters,G.J.; Abramson,R.D.;
Mullahy,S.J.; Bosak,S.A.; McEwan,P.J.; McKernan,K.J.;
Malek,J.A.; Gunaratne,P.H.; Richards,S.; Worley,K.C.;
Hale,S.; Garcia,A.M.; Gay,L.J.; Hulyk,S.W.;
Villalon,D.K.; Muzny,D.M.; Sodergren,E.J.; Lu,X.;
Gibbs,R.A.; Fahey,J.; Helton,E.; Ketteman,M.; Madan,A.;
Rodrigues,S.; Sanchez,A.; Whiting,M.; Madan,A.;
Young,A.C.; Shevchenko,Y.; Bouffard,G.G.;
Blakesley,R.W.; Touchman,J.W.; Green,E.D.;
Dickson,M.C.; Rodriguez,A.C.; Grimwood,J.; Schmutz,J.;
Myers,R.M.; Butterfield,Y.S.; Krzywinski,M.I.;
Skalska,U.; Smailus,D.E.; Schnurch,A.; Schein,J.E.;
Jones,S.J.; Marra,M.A.

TITLE (TI): Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903 (2002)

OTHER SOURCE (OS): CA 138:131969

REFERENCE: 2 (bases 1 to 1872)

AUTHOR (AU): Strausberg,R.

TITLE (TI): Direct Submission

JOURNAL (SO):

Submitted (09-JUN-2003) National Institutes of Health,
 Mammalian Gene Collection (MGC), Cancer Genomics
 Office, National Cancer Institute, 31 Center Drive,
 Room 11A03, Bethesda, MD 20892-2590, USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1872	/organism="Homo sapiens" /mol-type="mRNA" /db-xref="taxon:9606" /clone="MGC:61485 IMAGE:6162863" /tissue-type="skin, melanotic melanoma." /clone-lib="NIH-MGC-72" /lab-host="DH10B" /note="Vector: pCMV-SPORT6" /gene="GRB14" /db-xref="LocusID:2888" /db-xref="MIM:601524"
gene	1..1872	
CDS	12..1634	/codon-start=1 /product="growth factor receptor-bound protein 14" /protein-id="AAH53559.1" /db-xref="GI:31657224" /db-xref="LocusID:2888" /translation="MTTSLQDGQSAASRAAARDS PLAAQVCQAAQGRGDAHDLAPAPW LHARALLPLPDGTRGCAADRRKKKLDVPEMPSI PNPFPELCCSPFTSVLSADLFPKA NSRKKQVIKVSEDETSRALDVPSDITARDVCQL LILKNHYIDDHSWTLEFEHLPHIGV ERTIEDHELVIEVLSNWGIEEENKLYFRKNYAKY EFFKNPMYFFPEHMVSFATETNGE ISPTQILQMFLSSSTYPEIHGFLHAKEQGKKSWK KIYFFLRRSGLYFSTKGTSEPRH LQFFSEFGNSDIYVSLAGKKHGAPTNYGFCFKP NKAGGPRDLKMLCAEEEQSRCTCWV TAIRLLKYGMQLYQNYMHPYQGRSGCSSQSISPM RSISENSLVAMDPSGQKSRSVIENP TEALSVAVEEGLAWRKKGCLRLGTHGSPTASSQS SATNMAIHRSPWFFHKISRDEAQ RLIIQQGLVDGVFLVRDSQSNSPKTFVLSMSHGQK IKHFQIIPVEDDGEFMHTLDDGHT RFTDLIQLVEFYQLNKGVLPCKLHYCARIAL" /note="RA; Region: Ras association (RalGDS/AF-6) domain" /db-xref="CDD:smart00314"
misc-feature	327..587	/note="PH; Region: Pleckstrin homology domain" /db-xref="CDD:smart00233"
misc-feature	714..1031	/note="SH2; Region: src homology 2 domains" /db-xref="CDD:cd00173"
misc-feature	1323..1616	

SEQUENCE (SEQ):

1 ggcggcgcac aatgaccact tccctgcaag atggcagag cggcgcgagc agggcggtg
 61 cccgggattc gccgctggcc gcccagggtgt gtggcgtgc ccaggggagg ggcgacgccc
 121 acgacctggc gccggcccccc tggctgcacg cgcgagcgct cctgcccctt ccggacggga
 181 cccggggctg tgctgcagac aggaaaaaaa agaaagatct ttagttccg gaaatgccat
 241 ctattccaaa ccctttcct gagctatgct gttctccatt tacatctgtt ttgtcagcag
 301 acctatttcc caaagcaaatt tcaaggaaaa aacaggtgat taaagtatac agtgaagatg
 361 aaaccagcag ggcttttagat gtacccagtg acataacggc tcgagatgtt tgtcagctgt
 421 tgatcctgaa gaatcattac attgatgacc acagctggac cctttttgag cacctgcctc
 481 acatagggtt agaaagaaca atagaagacc acgaactggt gattgaagtg ctatccaact
 541 gggggataga agaagaaaaac aaactatact tttagaaaaaa ttatgccaaa tatgagttct
 601 ttaaaaaccc aatgtatttt ttcccgagc atatggatc ttttgcact gaaaccaatg
 661 gtgaaatatac ccccacacag atttcgaga tggatcgat ttcaaggcaca tatcctgaaa
 721 ttcatggttt cttacatgcg aaagaacagg gaaagaatgc ttggaaaaaaa atttactttt
 781 ttcaagaag atctggttt tatttttca ctaaaggaaac atcaaaaggaa cccggcatt
 841 tgcagtttt cagcgaattt ggcaatagtg atatttatgt gtcactggca ggcaaaaaaaa
 901 aacatggagc accgactaacatggattct gctttaagcc taacaaagcg ggagggcccc
 961 gagacctgaa aatgtctgtt gcaagaagaag agcagatgt gacgtgctgg gtgaccgcga
 1021 ttagattgct taagtatggc atgcagctgtt accagaatta tatgcattca tatcaaggt
 1081 gaagtggctg cagttcacag agcatatcac ctatgagaag tatatcagag aattccctgg
 1141 tagcaatgga cttctcaggc cagaaaagca gagttataga aatccact gaagcccttt

1201 cagttgcggg tgaagaagga ctcgcttggg ggaaaaaaagg atgtttacgc ctgggactc
 1261 acggtagccc cactgcctct tcacagagct ctgccacaaa catggctatc caccggtccc
 1321 accatgggtt tcaccacaaa attcttagag atgaggctca gcgattgtatt attcagcaag
 1381 gacttggaa tggagtttc ttggtagggg atagtcagag taaccccaaa actttcgatc
 1441 tgtcaatgag tcatggacaa aaaataaagc actttcaat tataccagta gaagatgacg
 1501 gtgaaatgtt ccacacactg gatgtatggcc acacaagatt tacagatcta atacagctgg
 1561 tggagttcta tcaactcaat aaggcggtt ttccttgaa gttgaaacat tattgtgcta
 1621 ggattgctct ctagacaagc cagaagtgc ttattaaact attgaaggaa aaggactcaa
 1681 gaaaaataat aaaagaccat aaataaggc gaaaacatta ccatgtgaaa agaatgtatt
 1741 tcacctgaa gttacaaaaa aatagttgt gcattgaaa taagcaaaga cttggattga
 1801 ctttacattc atcattaaa attcattagt taattaaa ccttaggaaa aaaaatgaaaa
 1861 aaaaaaaaaaa aa

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LOCUS (LOC): AK074599 GenBank (R)
 GenBank ACC. NO. (GBN): AK074599
 GenBank VERSION (VER): AK074599.1 GI:22760142
 CAS REGISTRY NO. (RN): 453084-12-3
 SEQUENCE LENGTH (SQL): 1513
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Primates
 DATE (DATE): 3 Sep 2002
 DEFINITION (DEF): Homo sapiens cDNA FLJ90118 fis, clone HEMBA1006916,
 highly similar to Homo sapiens ***Grb14*** mRNA.
 SOURCE: Homo sapiens embryo, 10 weeks whole embryo, mainly head
 cDNA to mRNA, clone_lib:HEMBA1 clone:HEMBA1006916.
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo
 NUCLEIC ACID COUNT (NA): 432 a 399 c 346 g 336 t
 COMMENT:

NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology; cDNA library construction:
 Institute of Medical Science, University of Tokyo, Laboratory of
 Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass
 sequencing and clone selection: Helix Research Institute (supported
 by Japan Key Technology Center etc.).

REFERENCE:
 AUTHOR (AU): 1 Isogai,T.; Ota,T.; Nishikawa,T.; Hayashi,K.; Otsuki,T.;
 Sugiyama,T.; Suzuki,Y.; Nagai,K.; Sugano,S.; Ishii,S.;
 Kawai-Hio,Y.; Saito,K.; Yamamoto,J.; Wakamatsu,A.;
 Nakamura,Y.; Kojima,S.; Nagahari,K.; Masuho,Y.; Ono,T.;
 Okano,K.; Yoshikawa,Y.; Aotsuka,S.; Sasaki,N.;
 Hattori,A.; Okumura,K.; Iwayanagi,T.; Ninomiya,K.
 TITLE (TI): NEDO human cDNA sequencing project
 JOURNAL (SO): Unpublished
 REFERENCE: 2 (bases 1 to 1513)
 AUTHOR (AU): Isogai,T.; Otsuki,T.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (25-MAR-2002) Takao Isogai, Helix Research
 Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu,
 Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp,
 Tel:81-438-52-3975, Fax:81-438-52-3986)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1513	<code>/organism="Homo sapiens"</code> <code>/db-xref="taxon:9606"</code> <code>/clone="HEMBA1006916"</code> <code>/tissue-type="whole embryo, mainly head"</code> <code>/clone-lib="HEMBA1"</code> <code>/dev-stage="embryo, 10 weeks"</code> <code>/note="cloning vector: pME18SFL3"</code>

SEQUENCE (SEQ):

1 tggctgcagt tcacagagca tatcacctat gagaagtata tcagagaatt ccctggtagc
 61 aatggacttc tcaggccaga aaagcagagt tatagaaaat cccactgaag ccctttcagt
 121 tgcggttgaa gaaggactcg ctggaggaa aaaaggatgt ttacgcctgg gcactcacgg
 181 tagccccact gcctcttcac agagctctgc cacaacatg gctatccacc ggtcccagcc
 241 atggtttcac cacaaaattt cctccgcccc ctccccccc ccgcgcctc gcagatagct
 301 cggccgcgcg tctcagccgc cggggccccg agcgcaggcg gcgaggccac cacacctgca

361 gagcgctcg gctgcctagg cgccacctcg cctcccgccg cggaaacccc ttctccccac
 421 gcccggagtc tcccatgacg cccgagcccc cggccggcg acaatgacca cttccctgca
 481 agatgggcag agcggcgca gcaggcgcc tgcccgat tagccgctgg cggcccggt
 541 gtgtggcgct gcccaggga ggggcgacgc ccacgacctg gcccggccc cttggctgca
 601 cgcgcgagcg ctccctgcccc ttccggacgg gaccggcgc tttgtctgcag acaggagaaa
 661 aaagaaaatgtt cttgatgttc cgaaaatgcc atctattcca aacccttttc ctgagctatg
 721 ctgttctcca attacatctg tttgtcagc agacctatcc cccaaagcaa attcaaggaa
 781 aaaacagggtg attaaagtat acagtgaaga taaaaccgc aggcttttag atgtacccag
 841 tgacataacg gtcgagatg tttgtcagct gttgatctg aagaatcatt acattgtga
 901 ccacagctgg acccttttg agcacctgca tcacatagggt gtagaaagaa caatagaaga
 961 ccacgaactg gtgatttgg ttttatccaa ctggggata gaagaagaaa acaaactata
 1021 ctttagaaaaa aattatgcca aatatgagtt cttaaaaac ccaatgtatt tttttccaga
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 1141 gattttctg agttcaagca catatcctga aatgttccac aactggatg atggccacac
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 1261 ttgcaagttt aacatttattt gtgcttaggt ttttcttag acaagccaga agtacttat
 1321 taaactattt aaggaaaagg actcaagaaa aataataaaa gaccataaat aagggcgaaa
 1381 acattatcat gtgaaaagaa ttttccatc ctgcaagttt caaaaaataa gtttgcatt
 1441 tacaataaag caaagactt gattgactttt acattcatca tttttttttt attagttaaa
 1501 attaaacctt agg

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LOCUS (LOC): BC021820 GenBank (R)
 GenBank ACC. NO. (GBN): BC021820
 GenBank VERSION (VER): BC021820.1 GI:18256069
 CAS REGISTRY NO. (RN): 387318-13-0
 SEQUENCE LENGTH (SQL): 870
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Rodents
 DATE (DATE): 16 Apr 2003
 DEFINITION (DEF): Mus musculus growth factor receptor bound protein 14,
 mRNA (cDNA clone IMAGE:3967891), partial cds.
 SOURCE: Mus musculus (house mouse)
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus
 NUCLEIC ACID COUNT (NA): 277 a 183 c 209 g 201 t
 COMMENT:

Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cDNA/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulsegod, H.,
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
 A.N., Gibbs, R.A.
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 40 Row: g Column: 24.

REFERENCE: 1 (bases 1 to 870)
 AUTHOR (AU): Strausberg, R.L.; Feingold, E.A.; Grouse, L.H.;
 Derge, J.G.; Klausner, R.D.; Collins, F.S.; Wagner, L.;
 Shenmen, C.M.; Schuler, G.D.; Altschul, S.F.; Zeeberg, B.;
 Buetow, K.H.; Schaefer, C.F.; Bhat, N.K.; Hopkins, R.F.;
 Jordan, H.; Moore, T.; Max, S.I.; Wang, J.; Hsieh, F.;
 Diatchenko, L.; Marusina, K.; Farmer, A.A.; Rubin, G.M.;
 Hong, L.; Stapleton, M.; Soares, M.B.; Bonaldo, M.F.;
 Casavant, T.L.; Scheetz, T.E.; Brownstein, M.J.;
 Usdin, T.B.; Toshiyuki, S.; Carninci, P.; Prange, C.;
 Raha, S.S.; Loquellano, N.A.; Peters, G.J.; Abramson, R.D.;
 Mullahy, S.J.; Bosak, S.A.; McEwan, P.J.; McKernan, K.J.;
 Malek, J.A.; Gunaratne, P.H.; Richards, S.; Worley, K.C.;
 Hale, S.; Garcia, A.M.; Gay, L.J.; Hulyk, S.W.;
 Villalon, D.K.; Muzny, D.M.; Sodergren, E.J.; Lu, X.;
 Gibbs, R.A.; Fahey, J.; Helton, E.; Ketteman, M.; Madan, A.;
 Rodrigues, S.; Sanchez, A.; Whiting, M.; Madan, A.;
 Young, A.C.; Shevchenko, Y.; Bouffard, G.G.;
 Blakesley, R.W.; Touchman, J.W.; Green, E.D.;
 Dickson, M.C.; Rodriguez, A.C.; Grimwood, J.; Schmutz, J.;

Myers, R.M.; Butterfield, Y.S.; Krzywinski, M.I.;
 Skalska, U.; Smailus, D.E.; Schnerech, A.; Schein, J.E.;
 Jones, S.J.; Marra, M.A.
TITLE (TI): Generation and initial analysis of more than 15,000
 full-length human and mouse cDNA sequences
JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903
 (2002)
OTHER SOURCE (OS): CA 138:131969
REFERENCE: 2 (bases 1 to 870)
AUTHOR (AU): Strausberg, R.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (18-JAN-2002) National Institutes of Health,
 Mammalian Gene Collection (MGC), Cancer Genomics
 Office, National Cancer Institute, 31 Center Drive,
 Room 11A03, Bethesda, MD 20892-2590, USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..870	<i>/organism="Mus musculus"</i> <i>/mol-type="mRNA"</i> <i>/strain="FVB/N"</i> <i>/db-xref="taxon:10090"</i> <i>/clone="IMAGE:3967891"</i> <i>/tissue-type="Mammary tumor.</i> <i>Metallothionein-TGF alpha model.</i> <i>10 month old virgin mouse. Taken</i> <i>by biopsy."</i> <i>/clone-lib="NCI-CGAP-Mam1"</i> <i>/lab-host="DH10B"</i> <i>/note="Vector: pCMV-SPORT6"</i>
gene	<1..870	<i>/gene="Grb14"</i> <i>/db-xref="LocusID:50915"</i> <i>/db-xref="MGI:1355324"</i>
CDS	<1..625	<i>/gene="Grb14"</i> <i>/codon-start=2</i> <i>/product="Grb14 protein"</i> <i>/protein-id="AAH21820.1"</i> <i>/db-xref="GI:18256070"</i> <i>/db-xref="LocusID:50915"</i> <i>/db-xref="MGI:1355324"</i> <i>/translation="VTAIRLLKDGMQLYQNYMHP</i> <i>YQGRSACNSQSMSMRSVSENSLV</i> <i>AMDFSGEKSRSVIDNPTEALSVAVEEGLAWRKKG</i> <i>LRLGNHGSPSAPSQSSAVNMALHR</i> <i>SQPWFHHRISRDEAQRLIIRQGPVDGVFLVRDSQ</i> <i>SNPRTFVLSMSHGQKIKHYQIIPV</i> <i>EDDGELFHTLDDGHTKFTDLIQLVEFYQLNRGVL</i> <i>PCKLKHYCARMAV"</i>

SEQUENCE (SEQ):

1 ggtgaccgcc atccgactgc tgaaggatgg catgcagctg tatcagaatt atatgcatcc
 61 ataccaagggt agaagcgccct gcaattctca gagcatgtca cccatgagaa gcgtatcaga
 121 gaattcccta gtagcaatgg acttctcagg tgagaagagc agagtcata gacaacccac
 181 tgaagcgctt tcgggtgctg ttgaggaagg cctcgcgtgg agaaaaaaag gctgtttacg
 241 cctggggaat cacggaaagcc ccagtgc(ccc ctcggagac tctgctgtga acatggctct
 301 ccatcggtcc caaccatggt ttaccacag aatttccaga gatgaggcgtc agcggctgat
 361 cattcgccag gggctgtgg atggagttt cttggtaggg gatagtcaga gtaacccag
 421 aactttgtt ctgtcaatga gtcattggaca aaagataaaa cactatcaaa ttatacccg
 481 agaagatgtat ggtgagctgt tccatactct ggatgatggc catacgaagt tcacagac
 541 catccagctg gtggagttct accagctcaa caggggggtc cttccttgca agctgaagca
 601 ttactgtgtt aggtatggctg tttagccaaa ctgtgtgtca ctcgttacac tacagaagaa
 661 gaaggatgca aaggagaatg attagagaga gagagagaga tcacaaggct gaaaacaat
 721 catggtgaaa agaagatttc acctgcgggt tacaaaaaaa aataggtcac acattgcaaa
 781 tttagtggaaaa cttggattcc tattacactc atgactttaa atttattatgt taaaattaaa
 841 ctttattaaa aaaataaaaaa aaaaaaaaaa

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LOCUS (LOC): AF329696 **GenBank (R)**
GenBank ACC. NO. (GBN): AF329696
GenBank VERSION (VER): AF329696.1 GI:13161041
CAS REGISTRY NO. (RN): 325452-27-5
SEQUENCE LENGTH (SQL): 3815
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Primates

DATE (DATE): 14 May 2001
 DEFINITION (DEF): Homo sapiens tankyrase 2 mRNA, complete cds.
 SOURCE: human.
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo
 NUCLEIC ACID COUNT (NA): 1120 a 788 c 924 g 983 t
 REFERENCE:
 AUTHOR (AU): Lyons,R.J.; Deane,R.; Lynch,D.K.; Ye,Z.S.;
 Sanderson,G.M.; Eyre,H.J.; Sutherland,G.R.; Daly,R.J.
 TITLE (TI): Identification of a novel human tankyrase through its
 interaction with the adaptor protein ***Grb14***
 JOURNAL (SO): J. Biol. Chem., 276 (20), 17172-17180 (2001)
 OTHER SOURCE (OS): CA 135:118599
 REFERENCE:
 AUTHOR (AU): Lyons,R.J.; Deane,R.; Lynch,D.K.; Ye,Z.-S.J.;
 Sanderson,G.M.; Eyre,H.J.; Sutherland,G.R.; Daly,R.J.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (17-DEC-2000) Cancer Research, Garvan
 Institute of Medical Research, 384 Victoria St.,
 Sydney, NSW 2010, Australia

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..3815	/organism="Homo sapiens" /db-xref="taxon:9606" /chromosome="10" /map="10q23.2"
CDS	140..3640	/codon-start=1 /product="takyrase 2" /protein-id="AAK13463.1" /db-xref="GI:13161042" /translation="MSGRRCAAGGAACASAAEA VEPAARELFEACRNGDVERVKRLV TPEKVNSRDTAGRSTPLHFAAGFGRKDVEYLL QNGANVQARDDGGIPLHNACSGF HAEVNLLRHGADPNARDNWNYTPLHEAAIKGK IDVCIVLQHGAEPDIRNTDRTA LDLADPSAKAVLTGEYKKDELLESARSGNEEKMM ALLTPLNVNCHASDGRKSTPLH AGYNRVKIVQLLQHGADVHAKDKGDLVPLHNAC SYGHYEVTELLVKGACVNAMDLW QFTPLHEAASKNRVEVCSLLSYGADPTLLNCHN KSAIDLAPTPQLKERLAYEFGKHS LLQAAREADVTRIKKHSLEMVNFKHPQTHTAL HCAAASPYPKRKQICELLRKGAN INEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV NALDNLGQTSLHRAAYCGHLQTCR LLLSYGCDPNIISLQGFTALQMGNENVQQLQEG ISLGNSEADRQLLEAAKAGDVETV KKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVV EYLLQHGADVHAKDKGGLVPLHNA CSYGHYEVAEELLVKGAVVNADLWKFTPLHEAA AKGKYEICKLLLQHGADPTKKNRD GNTPLDLVKDGTDIQLLRGDAALLDAAKKGCL ARVKKLSSPDNVNCRDTQGRHSTP LHLAAGYNNLEVAEYLLQHGADVNAQDKGGIPL HNAASYGHVDVAALLIKYNACVNA TDKWAFTPLHEAAQKGRQLCALLLAHGADPTLK NQEQTPLDLVSADDVSALLTAAM PPSALPSCYKPQVNGVRSPGATADALSSGPSSP SSLSSAASSLDNLNGSFSELSSVVS SSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHL MDIFEREQITLDVLVEMGHKELKE IGINAYGHRHKLIKGVRLISGQQGLNPYLTNT SGSGTILIDLSPDDEKFQSVEEEM QSTVREHRDGGHAGGIIFNRYNILKIQKVCNKKLW ERYTHRKEVSEENHNHANERMLF HGSPFVNIAIIHKGFDERHAYIGGMFGAGIYFAEN SSKSNQYVYGGGGTGPVHKDRS CYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGH HVTGRPSVNGLALAEEYVIYRGEQ AYPEYLITYQIMRPEGMVDG"

SEQUENCE (SEQ):

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 61 cctcgccctc ctgctcgccg gggcggggct cctgctccgg ttgctggcgc tggtgctggc
 121 tgtggcggcg gccaggatca tgtcggtcg cgcgtcgcc ggcgggggag cggctgcgc
 181 gagcgcgcg gccgaggccg tgagccggc cgcccgagag ctgttcgagg cgtgcgcgaa
 241 cggggacgtg gaacgagtca agaggctgtt gacgccttag aaggtgaaca gccgcacac
 301 ggcggcagg aaatccaccc cgctgactt cgccgcagg tttggcggaa aagacgtagt
 361 tgaatatttgc ttcaagaatgt gtgcaaatgtt ccaagcacgt gatgtgggg gccttattcc
 421 tcttcataat gcatgctctt ttggcatgc tgaagtagtc aatctcctt tgcacatgg
 481 tgcagacccc aatgctcgag ataattggaa ttatactcctt ctccatgaag ctgcaattaa
 541 agggaaagatt gatgttgca ttgtgtgtt acagcatgaa gctgagccaa ccattccgaaa
 601 tacagatgga aggacagcat tgatgttgc agatccatct gccaaagcag tgcttactgg
 661 tgaatataag aaagatgaaac tcttagaaag tgccaggagt ggcaatgaag aaaaaatgtat
 721 ggctctactc acaccattaa atgtcaactg ccacgcaagt gatggcagaa agtcaactcc
 781 attacatttg gcagcaggat ataacagagt aaagattgtt cagctgttac tgcaacatgg
 841 agctgatgtc catgctaaag ataaagggtga tctggtacca ttacacaatg cctgttctta
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 1261 tccatatccc aaaagaaagc aaatatgttca actgttgctt agaaaaggag caaacatcaa
 1321 tgaaaagact aaagaattct tgactccctc gcacgtggca tctggagaaag ctcatatga
 1381 tgggttggaa gtaggtgtt aacatgaaagc aaaggtaat gctctggata atcttggtca
 1441 gacttctcta cacagagctg catattgtgg tcatctacaa acctgccc tttcttgag
 1501 ctatgggtgt gatcctaaat ttatccctt tcagggtttt actgttttac agatgggaaa
 1561 tgaaaatgtt cagaacttcc tccaagggg tatcttattt ggttaatttca aggcagacag
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 1861 tgcagaactt cttgtttaaac atggagctgtt agttatgtt gctgttttattt gaaatttac
 1921 acctttatcat gaagcagcag caaaaggaaa atatgaaattt tgcacactt tgcctcagca
 1981 tggtcagac cttacaaaaaa aaaacaggaa tggaaatactt ccttggatc ttgtttaaaga
 2041 tggagataca gatattcaat atctgtttttag gggagatgttca gctttgtttagt atgctgc
 2101 gaagggttgg ttagccagag tgaagaatgtt gtttttttccat gataatgttatttgc
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 2281 tcctttatcat aatgcagcat cttacggggca ttttgcatttgc gtttttttccat taaaatgt
 2341 taatgcattt gtcacatgttcc cggacaaatg ggcttttccat ctttgcacgg aacccatcc
 2401 aaaggggacga acacagctt gtttttttccat gtttttttccat gtttttttccat taaaatgt
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 2521 gacagcagcc atgccccat ctgttgcaccc ctgttgcattt gtttttttccat taaaatgt
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 2821 tgagagagaa ctttttttccat ttttgcattt gtttttttccat taaaatgt
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 2941 ctccggacaaat ctttttttccat ttttgcattt gtttttttccat taaaatgt
 3001 tctttagat ttttgcattt gtttttttccat ttttgcattt gtttttttccat taaaatgt
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 3721 aaaaaaaaaatc atcttgcaccc ctttttttccat taaaatgt
 3781 acattctgttca ttttgcattt gtttttttccat taaaatgt

L6 ANSWER 80 OF 135

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LOCUS (LOC): BB560608 GenBank (R)

GenBank ACC. NO. (GBN): BB560608

GenBank VERSION (VER): BB560608.1 GI:9646974

CAS REGISTRY NO. (RN): 284994-84-9

SEQUENCE LENGTH (SQL): 323

MOLECULE TYPE (CI): mRNA; linear

DIVISION CODE (CI): Expressed sequence tag

DATE (DATE): 1 Aug 2000

DEFINITION (DEF): BB560608 RIKEN full-length enriched, 10 days neonate, olfactory brain *Mus musculus* cDNA clone E530113B02 3' similar to AF076619 *Rattus norvegicus* molecular adapter rGrb14 (***Grb14***) mRNA, mRNA sequence.

SOURCE: house mouse.

ORGANISM (ORGN): *Mus musculus*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; *Mus*

NUCLEIC ACID COUNT (NA): 92 a 89 c 53 g 89 t

COMMENT:

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,

URL:<http://genome.gsc.riken.go.jp/>

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome rtc.riken.go.jp>) for further details.

REFERENCE:

AUTHOR (AU):

1 (bases 1 to 323)

Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.; Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.; Kikuchi,N.; Kirosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.; Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.; Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.y; Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.; Shibata,Y.; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.; Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.; Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a; Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.; Yamanaka,I.; Yano,R.H.; Yasunishi,A.; Yokota,T.; Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.; Hayashizaki,Y.

TITLE (TI):

RIKEN Mouse ESTs (Konno,H., et al.)

JOURNAL (SO):

Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..323	/organism="Mus musculus" /db-xref="taxon:10090" /clone="E530113B02" /clone-lib="RIKEN full-length enriched, 10 days neonate olfactory brain" /tissue-type="olfactory brain" /dev-stage="10 days neonate" /lab-host="DH10B" /note="Site-1: SalI; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken"

contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGCGGCCGCACTCGAGTTTTTT TTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

SEQUENCE (SEQ):

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121 cactacaga gaagaagcat ccaaaggagt atgataacag agagagagag agatcaccag
181 gctaaaacc catcatggt gaaaggagat ttcaccccg ggttacccaa acaaatacggt
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301 agttaaaatt aaaccctttt aac

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L6 ANSWER 81 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB560607 GenBank (R)
 GenBank ACC. NO. (GBN): BB560607
 GenBank VERSION (VER): BB560607.1 GI:9646973
 CAS REGISTRY NO. (RN): 284994-83-8
 SEQUENCE LENGTH (SQL): 313
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 1 Aug 2000
 DEFINITION (DEF): BB560607 RIKEN full-length enriched, 10 days neonate olfactory brain *Mus musculus* cDNA clone E530113B01 3' similar to AF076619 *Rattus norvegicus* molecular adapter rGrb14 (***Grb14***) mRNA, mRNA sequence.
 SOURCE: house mouse.
 ORGANISM (ORGN): *Mus musculus*
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; *Mus*
 NUCLEIC ACID COUNT (NA): 100 a 76 c 54 g 83 t
 COMMENT:

Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,
 URL: <http://genome.gsc.riken.go.jp/>
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome rtc.riken.go.jp>) for further details.

REFERENCE: 1 (bases 1 to 313)

AUTHOR (AU): Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.; Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.; Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.; Hori, F.; Ishii, Y.; Ishikawa, J.; Ishikawa, T.; Itoh, M.;

Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.;
 Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.;
 Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.;
 Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y., Ono,T.y;
 Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.;
 Shibata,Y., Shigemoto,Y.; Shinagawa,A.; Shiraki,T.;
 Sogabe,Y.; Sugahara,Y., Suzuki,H.; Suzuki,H.;
 Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a;
 Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.;
 Yamanaka,I., Yano,R.H.; Yasunishi,A.; Yokota,T.;
 Yoshida,K.; Yoshiki,A.; Yoshino,M..; Muramatsu,M.;
 Hayashizaki,Y.

TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al.)
 JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..313	/organism="Mus musculus" /db-xref="taxon:10090" /clone="E530113B01" /clone-lib="RIKEN full-length enriched, 10 days neonate olfactory brain" /tissue-type="olfactory brain" /dev-stage="10 days neonate" /lab-host="DH10B" /note="Site-1: SalI; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGCGGCCGCACTCGAGTTTTTTT TTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTC CCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

SEQUENCE (SEQ):

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1 ccacctatat ccagttggtg gacttccacc agcttaacag gcggccttc cttccacat
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121 gaagaagaag gattctaagg agaatgtca gagagagaga gagagatcac aaggctgcaa
181 acatatcatg ctgaaaagga gattcacct gcgggttacc aaaaaaaaaa ggtcacacat
241 tccaaattag tgcaaacttg gattcctatt acactcatga cttaaattt attagttaaa
301 attaaacctt att

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L6 ANSWER 82 OF 135

GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB559554 GenBank (R)
 GenBank ACC. NO. (GBN): BB559554
 GenBank VERSION (VER): BB559554.1 GI:9645920
 CAS REGISTRY NO. (RN): 284984-30-1
 SEQUENCE LENGTH (SQL): 334
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 1 Aug 2000
 DEFINITION (DEF): BB559554 RIKEN full-length enriched, 2 days pregnant
 adult female ovary Mus musculus cDNA clone E330039G15
 3' similar to AF076619 Rattus norvegicus molecular
 adapter rGrb14 (***Grb14***) mRNA, mRNA sequence.

SOURCE: house mouse.
ORGANISM (ORGN): *Mus musculus*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; *Mus*
NUCLEIC ACID COUNT (NA): 117 a 90 c 41 g 86 t

COMMENT:

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,
URL:<http://genome.gsc.riken.go.jp/>

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)

Please visit our web site (<http://genome rtc.riken.go.jp>) for
further details.

REFERENCE: 1 (bases 1 to 334)

AUTHOR (AU): Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.;
Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.;
Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.;
Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.;
Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.;
Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.;
Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.y.;
Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.;
Shibata,Y.; shigemoto,Y.; Shinagawa,A.; Shiraki,T.;
Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.;
Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a.;
Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.;
Yamanaka,I.; Yano,R.H.; Yasunishi,A.; Yokota,T.;
Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.;
Hayashizaki,Y.

TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al.)

JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..334	/organism="Mus musculus" /db-xref="taxon:10090" /clone="E330039G15" /clone-lib="RIKEN full-length enriched, 2 days pregnant adult female ovary" /sex="female" /tissue-type="ovary" /dev-stage="2 days pregnant adult" /lab-host="DH10B" /note="Site-1: Sali; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'

GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTT
 TTTTTTTTVN 3'], cDNA was prepared
 by using trehalose
 thermo-activated reverse
 transcriptase and subsequently
 enriched for full-length by
 cap-trapper. Second strand cDNA
 was prepared with the primer
 adapter of sequence [5'
 GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC
 CCCCCCCCCC 3']. cDNA was cleaved
 with BamHI and XhoI. Vector: a
 modified pBluescript KS(+) after
 bulk excision from Lambda FLC I."

SEQUENCE (SEQ):

```

1 gtacttcaca tacatcatcc acctcttagac tttcaccaat ttccacaccc cttccttcc
61 ctttccaccc gaaccaccac tggccactga ttcccccctt ccccaacttt ctctcacttc
121 ctacactaca gaagaagaag gatccaaagg agaatcatta gagagagaga gagagatcac
181 aaggctgaaa accaatcatg gtgaaaagaa gattcacct ccggcttaca aaaacaaata
241 ggtcacacat tccaaattag taaaaacttg gattcctatt acactcatga ctttaattt
301 attagttaaa attaaacctt attaaaaaaa tagg

```

L6 ANSWER 83 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB559080 GenBank (R)
 GenBank ACC. NO. (GBN): BB559080
 GenBank VERSION (VER): BB559080.1 GI:9645446
 CAS REGISTRY NO. (RN): 284979-54-0
 SEQUENCE LENGTH (SQL): 319
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 1 Aug 2000
 DEFINITION (DEF): BB559080 RIKEN full-length enriched, 2 days pregnant
 adult female ovary *Mus musculus* cDNA clone E330037E03
 3' similar to AF076619 *Rattus norvegicus* molecular
 adapter rGrb14 (***Grb14***) mRNA, mRNA sequence.
 SOURCE: house mouse.
 ORGANISM (ORGN): *Mus musculus*
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; *Mus*

NUCLEIC ACID COUNT (NA): 108 a 62 c 62 g 87 t

COMMENT:

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 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center(GSC), Yokohama Institute
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Email: genome-res@gsc.riken.go.jp,
 URL:<http://genome.gsc.riken.go.jp/>
 Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
 ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Thermostabilization and thermoactivation of thermolabile enzymes by
 trehalose and its application for the synthesis of full length
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
 Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
 ,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)

Please visit our web site (<http://genome rtc.riken.go.jp>) for
 further details.

REFERENCE: 1 (bases 1 to 319)

AUTHOR (AU): Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
 Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.;
 Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.;
 Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.;
 Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.;
 Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.;
 Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.;

Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y., Ono,T.y;
Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.;
Shibata,Y.,; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.;
Sogabe,Y.; Sugahara,Y., Suzuki,H.,; Suzuki,H.;
Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a;
Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.;
Yamanaka,I., Yano,R.H; Yasunishi,A.; Yokota,T.;
Yoshida,K.; Yoshiki,A.; Yoshino,M..; Muramatsu,M.;
Hayashizaki,Y.

TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al.)
JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..319	/organism="Mus musculus" /db-xref="taxon:10090" /clone="E330037E03" /clone-lib="RIKEN full-length enriched, 2 days pregnant adult female ovary" /sex="female" /tissue-type="ovary" /dev-stage="2 days pregnant adult" /lab-host="DH10B" /note="Site-1: Sali; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGCGCCGCAACTCGAGTTTTTT TTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

SEQUENCE (SEQ):

1 tggttacaga cctgatccag ccgctggaaat tcaacccctt taactggggg tccttccttc
61 catgctgaag cattattctg cttaggacggc tggttatcccc aactttgttt cactcggtcac
121 actacagtag aagaaggatg caaaggagaa tgatttagaga gagagagaga gatcacaagg
181 ctgaaaacaa atcatggtga aaagaagatt tcacctgcgg gttacaaaaaa aaaataggtc
241 acacattgca aattagtgaa aacttggatt cctattacac tcatgacttt aaatttattt
301 gttaaaaatta aaccttattt

L6 ANSWER 84 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB558470 GenBank (R)
GenBank ACC. NO. (GBN): BB558470
GenBank VERSION (VER): BB558470.1 GI:9644836
CAS REGISTRY NO. (RN): 284973-44-0
SEQUENCE LENGTH (SQL): 250
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 1 Aug 2000
DEFINITION (DEF): BB558470 RIKEN full-length enriched, 2 days pregnant
adult female ovary *Mus musculus* cDNA clone E330034C06
3' similar to AF076619 *Rattus norvegicus* molecular
adapter rGrb14 (***Grb14***) mRNA, mRNA sequence.
house mouse.
SOURCE:
ORGANISM (ORGN): *Mus musculus*

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 74 a 54 c 49 g 73 t

COMMENT:

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Email: genome-res@gsc.riken.go.jp,

URL:<http://genome.gsc.riken.go.jp/>

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki ,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome rtc.riken.go.jp>) for further details.

REFERENCE: 1 (bases 1 to 250)

AUTHOR (AU):

Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.; Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.; Kikuchi,N.; Kirosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.; Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.; Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.y; Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.; Shibata,Y.; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.; Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.; Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a; Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.; Yamanaka,I.; Yano,R.H.; Yasunishi,A.; Yokota,T.; Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.; Hayashizaki,Y.

TITLE (TI):

RIKEN Mouse ESTs (Konno,H., et al.)

JOURNAL (SO):

Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..250	/organism="Mus musculus" /db-xref="taxon:10090" /clone="E330034C06" /clone-lib="RIKEN full-length enriched, 2 days pregnant adult female ovary" /sex="female" /tissue-type="ovary" /dev-stage="2 days pregnant adult" /lab-host="DH10B" /note="Site-1: Sali; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGCGGCCGCACTCGAGTTTTTT TTTTTTTVN 3'], cDNA was prepared

by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

SEQUENCE (SEQ):

1 ctttagcgc tgaaatgaat gctgacagat cccctacaca gatactgcag gtgttttaa
61 gctccagcac gtatcctgaa atccatggct tcttacatgc aaaggaacag gaaaagaagt
121 cttggaaaaaa agcttacttt tttctcagaa gatctggctt atatttttt actaaaggca
181 catccaagga accacggcat ttgcagctt tcagtgaatt cagcactagt cacgttata
241 tgtcactggc

L6 ANSWER 85 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB519321 GenBank (R)
GenBank ACC. NO. (GBN): BB519321
GenBank VERSION (VER): BB519321.1 GI:9570779
CAS REGISTRY NO. (RN): 284222-57-7
SEQUENCE LENGTH (SQL): 319
MOLECULE TYPE (CI): mRNA; Linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 28 Jul 2000
DEFINITION (DEF): BB519321 RIKEN full-length enriched, 16 days neonate heart Mus musculus cDNA clone D830035H10 3' similar to AF076619 Rattus norvegicus molecular adapter rGrb14 (***Grb14***) mRNA, mRNA sequence.
SOURCE: house mouse.
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 106 a 71 c 58 g 84 t
COMMENT:

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URL:<http://genome.gsc.riken.go.jp/>

Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome rtc.riken.go.jp>) for further details.

REFERENCE:
AUTHOR (AU): 1 (bases 1 to 319)
Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.;
Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.;
Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.;
Hori, F.; Ishii, Y.; Ishikawa, J.; Ishikawa, T.; Itoh, M.;
Izawa, M.; Kadota, K.; Kagawa, I.; Kai, C.; Kawai, J.;
Kikuchi, N.; Kiyosawa, H.; Kojima, Y.; Kondo, S.; Koya, S.;
Kurihara, C.; Kusakabe, M.; Matsuyama, T.; Miki, R.;
Mizuno, Y.; Nakamura, M.; Oda, H.; Okazaki, Y.; Ono, T. y;
Owa, C.; Saito, H.; Sakai, C.; Sato, K.; Shibata, K.;
Shibata, Y.; Shigemoto, Y.; Shinagawa, A.; Shiraki, T.;

Sogabe, Y.; Sugahara, Y., Suzuki, H.; Suzuki, H.;
Tagawa, A.; Takahashi, F.; Tominaga, N.; Toya, T.a;
Tsunoda, Y.; Watahiki, A.; Watanabe, S.; Yamamura, T.;
Yamanaka, I., Yano, R.H; Yasunishi, A.; Yokota, T.;
Yoshida, K.; Yoshiki, A.; Yoshino, M..; Muramatsu, M.;
Hayashizaki, Y.

TITLE (TI): RIKEN Mouse ESTs (Konno, H., et al.)
JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..319	/organism="Mus musculus" /db-xref="taxon:10090" /clone="D830035H10" /clone-lib="RIKEN full-length enriched, 16 days neonate heart" /tissue-type="heart" /dev-stage="16 days neonate" /lab-host="DH10B" /note="Site-1: Sali; site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGCGGGCGCAACTCGAGTTTTTTT TTTTTTTNTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTATTAAATTAATCC CCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

SEQUENCE (SEQ):

1 acttcacaga cctccttcca gctcggtggct tctaccagct caacaggggc tccttccctc
61 caagctgaac cattactttg ctaggatggc cgtttacccc aactttgtct cactcggtac
121 actacagaag aagaaggatc cataggagaa tgatcagaga gagagagaga gatcactagg
181 ctgaaaacaa atcatggtga aaagaagatt tcacctgcgg gttacaaaaaa ataataggta
241 acacattgca aattatgtaa aacttggatt cctattacac tcatgacttt aaatttatta
301 gttaaaaattt aacatttattt

L6 ANSWER 86 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB360808 GenBank (R)
GenBank ACC. NO. (GBN): BB360808
GenBank VERSION (VER): BB360808.1 GI:9072636
CAS REGISTRY NO. (RN): 279052-46-9
SEQUENCE LENGTH (SQL): 231
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 12 Jul 2000
DEFINITION (DEF): BB360808 RIKEN full-length enriched, adult male corpus
striatum Mus musculus cDNA clone C030049M20 3' similar
to AF076619 Rattus norvegicus molecular adapter rGrb14
(***Grb14***) mRNA, mRNA sequence.
SOURCE: house mouse.
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 87 a 45 c 38 g 61 t
COMMENT:

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Email: genome-res@gsc.riken.go.jp,
URL:<http://genome.gsc.riken.go.jp/>

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki ,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome rtc.riken.go.jp>) for further details.

REFERENCE:

AUTHOR (AU):

1 (bases 1 to 231)

Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.;
Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.;
Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.;
Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.;
Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.;
Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.;
Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.y;
Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.;
Shibata,Y.; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.;
Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.;
Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a;
Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.;
Yamanaka,I., Yano,R.H.; Yasunishi,A.; Yokota,T.;
Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.;
Hayashizaki,Y.

TITLE (TI):

JOURNAL (SO):

RIKEN Mouse ESTs (Konno,H., et al.)

Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..231	/organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="C030049M20" /clone-lib="RIKEN full-length enriched, adult male corpus striatum" /sex="male" /tissue-type="corpus striatum" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: Sali; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGGATCCAAGAGCTTTTTTTT TTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by

cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTC CCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"

SEQUENCE (SEQ):

1 cctgttcagc ccaactctgt ctcaactccct acactacaga agaagaagga ttcacagggt
61 tatgattaga gagagaaaaga gagatcacaa ggctaaaaac aatcatgggt gtaaagaaga
121 tttcacctgc ggcttaccaa aaaaaatagg tcacacattc caaattatgt aaaacttgga
181 ttccttattac actcatgact ttaaatttat tagttaaaat taaaccttat t

L6 ANSWER 87 OF 135

GENBANK.RTM. COPYRIGHT 2004 ON STN

LOCUS (LOC): BB360354 GenBank (R)
GenBank ACC. NO. (GBN): BB360354
GenBank VERSION (VER): BB360354.1 GI:9072182
CAS REGISTRY NO. (RN): 279047-92-6
SEQUENCE LENGTH (SQL): 284
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 12 Jul 2000
DEFINITION (DEF): BB360354 RIKEN full-length enriched, adult male corpus striatum Mus musculus cDNA clone C030046J22 3' similar to AF076619 Rattus norvegicus molecular adapter rGrb14 (***Grb14***) mRNA, mRNA sequence.
SOURCE: house mouse.
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 103 a 53 c 54 g 74 t

COMMENT:

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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
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Email: genome-res@gsc.riken.go.jp,
URL:<http://genome.gsc.riken.go.jp/>

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome rtc.riken.go.jp>) for further details.

REFERENCE: 1 (bases 1 to 284)

AUTHOR (AU): Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.; Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.; Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.; Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.; Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.Y.; Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.; Shibata,Y.; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.;

Sogabe,Y.; Sugahara,Y., Suzuki,H.,; Suzuki,H.;
Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a;
Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.;
Yamanaka,I., Yano,R.H; Yasunishi,A.; Yokota,T.;
Yoshida,K.; Yoshiki,A.; Yoshino,M..; Muramatsu,M.;
Hayashizaki,Y.

TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al.)
JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..284	/organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="C030046J22" /clone-lib="RIKEN full-length enriched, adult male corpus striatum" /sex="male" /tissue-type="corpus striatum" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: SalI; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTTTTTTTT TTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTC CCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"

SEQUENCE (SEQ):

1 agctcaacag gggggtcctt ctttccaagc tgaaccatca ctgtgctagg atggctgttt
61 agccaaactt tctttcactc tttacactac agaagaagaa ggatccaaag gagaatgatt
121 agagagagag agagagatca caaggctgaa aacaaatcat ggtaaaaga agatttcacc
181 tccgggttac aaaaaaaaaat aggtcacaca ttgcaaatta gtgaaaactt ggattcctat
241 tacactcatg actttaaatt tattagttaa aattaaacct tatt

L6 ANSWER 88 OF 135

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LOCUS (LOC): BB359872 GenBank (R)
GenBank ACC. NO. (GBN): BB359872
GenBank VERSION (VER): BB359872.1 GI:9071700
CAS REGISTRY NO. (RN): 279043-10-6
SEQUENCE LENGTH (SQL): 245
MOLECULE TYPE (CI): mRNA; Linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 12 Jul 2000
DEFINITION (DEF): BB359872 RIKEN full-length enriched, adult male corpus
striatum Mus musculus cDNA clone C030043M21 3' similar
to AF076619 Rattus norvegicus molecular adapter rGrb14
(***Grb14***) mRNA, mRNA sequence.

SOURCE: house mouse.
ORGANISM (ORGN): *Mus musculus*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; *Mus*

NUCLEIC ACID COUNT (NA): 92 a 55 c 40 g 58 t

COMMENT:

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The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9222
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Email: genome-res@gsc.riken.go.jp,
URL:<http://genome.gsc.riken.go.jp/>

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
, Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)

Please visit our web site (<http://genome rtc.riken.go.jp>) for
further details.

REFERENCE: 1 (bases 1 to 245)

AUTHOR (AU): Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.;
Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.;
Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.;
Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.;
Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.;
Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.;
Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.y.;
Owa,C.; Saito,H.; Sakai,C.; Sato,K.; shibata,K.;
Shibata,Y., Shigemoto,Y.; Shinagawa,A.; Shiraki,T.;
Sogabe,Y.; Sugahara,Y.; Suzuki,H., Suzuki,H.;
Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a.;
Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.;
Yamanaka,I., Yano,R.H.; Yasunishi,A.; Yokota,T.;
Yoshida,K.; Yoshiki,A.; Yoshino,M..; Muramatsu,M.;
Hayashizaki,Y.

TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al.)

JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..245	/organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="C030043M21" /clone-lib="RIKEN full-length enriched, adult male corpus striatum" /sex="male" /tissue-type="corpus striatum" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: SalI; site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was

primed with a primer [5'
GAGAGAGAGAAGGGATCCAAGAGCTTTTTTT
TTTTTTTVN 3'], cDNA was prepared
by using trehalose
thermo-activated reverse
transcriptase and subsequently
enriched for full-length by
cap-trapper. cDNA went through one
round of normalization to Rot =
10.0 and subtraction to Rot =
185.0. Second strand cDNA was
prepared with the primer adapter
of sequence [5'
GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC
CCCCCCCCCCCC 3']. cDNA was cloned
into the XbaI and BamHI sites.
Vector: a modified pBluescript
KS(+) after bulk excision from
Lambda FLC I. Cloning sites, 5'
end: SalI; 3' end: BamHI"

SEQUENCE (SEQ):

1 accatccac gacgcccgt caccggact gtgtttcaact cgatacacca cagaagaaga
61 aggatccaa ggagaatgt tagagagaga gagagagatc acaaggctga aaacaaatca
121 tgctgaaaag aagatttac ctcgggtta caaaaaaaaaa tagttcacac attccaaatt
181 agtggaaact tggattccta ttacactt gactttaaat ttatttagtta aaattaaacc
241 ttatt

L6 ANSWER 89 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB319216 GenBank (R)
GenBank ACC. NO. (GBN): BB319216
GenBank VERSION (VER): BB319216.1 GI:9026251
CAS REGISTRY NO. (RN): 278502-24-2
SEQUENCE LENGTH (SQL): 311
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 11 Jul 2000
DEFINITION (DEF): BB319216 RIKEN full-length enriched, adult male corpora
quadrigemina Mus musculus cDNA clone B230379D24 3'
similar to AF076619 Rattus norvegicus molecular adapter
rGrb14 (***Grb14***) mRNA, mRNA sequence.
SOURCE: house mouse.
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 89 a 69 c 61 g 92 t
COMMENT:

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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
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Email: genome-res@gsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
, Y. and Hayashizaki, Y.

Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)

Please visit our web site (<http://genome rtc.riken.go.jp>) for
further details.

REFERENCE: 1 (bases 1 to 311)

AUTHOR (AU): Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.;
Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.;

Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.;
Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.;
Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.;
Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.;
Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.;
Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.y;
Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.;
Shibata,Y.; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.;
Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.;
Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a;
Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.;
Yamanaka,I.; Yano,R.H.; Yasunishi,A.; Yokota,T.;
Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.;
Hayashizaki,Y.

TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al.)
JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..311	/organism="Mus musculus" /db-xref="taxon:10090" /clone="B230379D24" /clone-lib="RIKEN full-length enriched, adult male corpora quadrigemina" /sex="male" /tissue-type="corpora quadrigemina" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: Sali; site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTTTTTTTT TTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

SEQUENCE (SEQ):

1 tatcccaaat tcgaattttt taagaacccc atgtatttct ttccagagca catgggtgtct
61 tttgcagctg aaatgaatgg tgacagatcc cctacacagg tactgcagg ttttttaagc
121 tccacgcacgt atccctgaaat ccacggcttc ttacatgcaa aggaacaggg aaagaagtct
181 tggaaaaaaag cttactttt tctcagaaga tctggctcat atttttctac taaaggcaca
241 tccaaaggAAC cacggcattt gcagtttgc agtgaattca gcactagtca cgtttatatg
301 tcactggcag g

LOCUS (LOC): BB283308 GenBank (R)

GenBank ACC. NO. (GBN): BB283308

GenBank VERSION (VER): BB283308.1 GI:8983757

CAS REGISTRY NO. (RN): 278048-97-8

SEQUENCE LENGTH (SQL): 503

MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 1 Aug 2000
DEFINITION (DEF): BB283308 RIKEN full-length enriched, adult retina *Mus musculus* cDNA clone A930101L21 3' similar to AF076619
Rattus norvegicus molecular adapter rGrb14 (***Grb14***) mRNA, mRNA sequence.

SOURCE: house mouse.
ORGANISM (ORGN): *Mus musculus*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; *Mus*

NUCLEIC ACID COUNT (NA): 162 a 97 c 113 g 131 t

COMMENT:

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,

URL:<http://genome.gsc.riken.go.jp/>

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome rtc.riken.go.jp>) for further details.

REFERENCE: 1 (bases 1 to 503)

AUTHOR (AU): Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.; Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.; Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.; Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.; Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.y.; Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.; Shibata,Y.; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.; Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.; Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a.; Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.; Yamanaka,I.; Yano,R.H.; Yasunishi,A.; Yokota,T.; Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.; Hayashizaki,Y.

TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al.)

JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..503	/organism="Mus musculus" /db-xref="taxon:10090" /clone="A930101L21" /clone-lib="RIKEN full-length enriched, adult retina" /tissue-type="retina" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: SalI; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in

RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTTTTTTTTT TTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAA TCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. ~Retina RNA was provided by Stefano Gustincich, Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA02115, USA, whose assistance we gratefully acknowledge

SEQUENCE (SEQ):

```

1 aggctcgccc gctgatcatt ccgcggggcc tctggatgga gttttcttgc tacggatgt
61 tcagagtaac cccagaacct ttgtactgtc aatgagtcat ggacaaaaga taaaacacta
121 tcaaattata cccgtagaag atgatggtga gctgtccat actctggatg atggccatac
181 gaagttcaca cacctcatcc agctgggtga gttctaccag ctcacacaggg gggtcctcc
241 ttgcaagctg aagcattact gtgctaggat ggctgtttag ccaaactgtt tgtcaactgt
301 tacactacag aagaagaagg atgcaaagga gaatgattag agagagagag agagatcaca
361 aggctgaaaa caaatcatgg tgaaaagaag atttcacctg cgggttacaa aaaaaaatag
421 gtcacacatt ccaaattagt gaaaacttgg attcctatta cactcatgac tttaaattta
481 gttagttaaa attaaacctt att

```

L6 ANSWER 91 OF 135

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LOCUS (LOC): BB282445 GenBank (R)
 GenBank ACC. NO. (GBN): BB282445
 GenBank VERSION (VER): BB282445.1 GI:8982894
 CAS REGISTRY NO. (RN): 278040-34-9
 SEQUENCE LENGTH (SQL): 281
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 1 Aug 2000
 DEFINITION (DEF): BB282445 RIKEN full-length enriched, adult retina *Mus musculus* cDNA clone A930037N11 3' similar to AF076619 *Rattus norvegicus* molecular adapter rGrb14 (***Grb14***) mRNA, mRNA sequence.
 SOURCE: house mouse.
 ORGANISM (ORGN): *Mus musculus* Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; *Mus*
 NUCLEIC ACID COUNT (NA): 92 a 86 c 37 g 66 t

COMMENT:

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 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp,
 URL: <http://genome.gsc.riken.go.jp/>
 Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki ,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. *Genome Res.* 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303, 19-44 (1999)

Please visit our web site (<http://genome rtc.riken.go.jp>) for further details.

REFERENCE: 1 (bases 1 to 281)

AUTHOR (AU):

Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.; Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.; Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.; Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.; Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.Y.; Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.; Shibata,Y.; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.; Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.; Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a; Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.; Yamanaka,I., Yano,R.H.; Yasunishi,A.; Yokota,T.; Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.; Hayashizaki,Y.

TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al.)

JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..281	/organism="Mus musculus" /db-xref="taxon:10090" /clone="A930037N11" /clone-lib="RIKEN full-length enriched, adult retina" /tissue-type="retina" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: sali; site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTTTTTTTT TTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5'GAGAGAGAGATTCTCGAGTTAATTAAATTAA TCCCCCCCCCCCC 3']. cDNA was cleaved with XbaI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. ~Retina RNA was provided by Stefano Gustincich, Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA02115, USA, whose assistance we

gratefully acknowledge

SEQUENCE (SEQ):

1 ccgtatccct tccatcccc a cctgatagta tccctccca tcccacgcct cccctcgccc
61 tacatcccc tcacttact acaccacaga gaagcaggat ccccccgcac aatcactaga
121 gagagagaga gagattaca cccgaaaac aaatcatgtt gacaagaaga ttttacccccc
181 gggttacaaa agaaaatagc tcacacattt caaattatgtt aaaaacttgga ttccttattac
241 attcatgact ttaaatttat tagttaaaat taaaccttac t

L6 ANSWER 92 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB191006 GenBank (R)
GenBank ACC. NO. (GBN): BB191006
GenBank VERSION (VER): BB191006.1 GI:8851625
CAS REGISTRY NO. (RN): 276734-11-3
SEQUENCE LENGTH (SQL): 276
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 30 Jun 2000
DEFINITION (DEF): BB191006 RIKEN full-length enriched, adult male spinal cord Mus musculus cDNA clone A330065D15 3' similar to AF076619 Rattus norvegicus molecular adapter rGrb14 (***Grb14***) mRNA, mRNA sequence.
SOURCE: house mouse.
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 97 a 62 c 45 g 72 t
COMMENT:

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:<http://genome.gsc.riken.go.jp/>
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (<http://genome rtc.riken.go.jp>) for further details.

REFERENCE: 1 (bases 1 to 276)

AUTHOR (AU): Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.; Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.; Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.; Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.; Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.y.; Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.; Shibata,Y.; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.; Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.; Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a.; Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.; Yamanaka,I.; Yano,R.H.; Yasunishi,A.; Yokota,T.; Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.; Hayashizaki,Y.

TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al.)
JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
-------------	----------	-----------

SEQUENCE (SEQ):

1 cctgggatcc ttcccattcaa gctgcaacat cactttgcta ggacgcccgt taaccccaac
61 tctgtttcac tcattacacc acagaaggag aaggatccaa aggagaatga ttagagagag
121 agagagagat cacaaggctg aaaacaattc atcgtaaaaa gcagatttca cctccggctt
181 accaaaataa atagttcaca cattccaaat tagtgaaaaac ttggattcct attacactca
241 tgactttaaa tttatttagtt aaaattaaac cttatt

L6 ANSWER 93 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB187252 GenBank (R)
GenBank ACC. NO. (GBN): BB187252
GenBank VERSION (VER): BB187252.1 GI:8847823
CAS REGISTRY NO. (RN): 276657-85-3
SEQUENCE LENGTH (SQL): 289
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 30 Jun 2000
DEFINITION (DEF): BB187252 RIKEN full-length enriched, adult male spinal cord Mus musculus cDNA clone A330041E09 3' similar to AF076619 Rattus norvegicus molecular adapter rGrb14 (***Grb14***) mRNA. mRNA sequence.

SOURCE: house mouse.
ORGANISM (ORGN): *Mus musculus*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; *Mus*

NUCLEIC ACID COUNT (NA): 105 a 51 c 58 g 75 t

COMMENT:

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URL:<http://genome.gsc.riken.go.jp/>

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome rtc.riken.go.jp>) for further details.

REFERENCE:

AUTHOR (AU):

1 (bases 1 to 289)

Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.; Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.; Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.; Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.; Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.y; Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.; Shibata,Y.; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.; Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.; Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a; Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.; Yamanaka,I.; Yano,R.H.; Yasunishi,A.; Yokota,T.; Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.; Hayashizaki,Y.

TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al.)

JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..289	/organism="Mus musculus" /db-xref="taxon:10090" /clone="A330041E09" /clone-lib="RIKEN full-length enriched, adult male spinal cord" /sex="male" /tissue-type="spinal cord" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: SalI; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTTTTTTTT TTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAAATCC CCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after

SEQUENCE (SEQ):

```

1 ttaccagctc aaaagggggc tccttccttg caagctgaac cataactgtg ctaggatggc
61 tgtttagcct tactctgtt cactcggtac actacagaag aagaaggatg caaaggagaa
121 tgatcagaga gagagagaga gatcacaagg ctgaaaacaa atcatggtga aaagaagatt
181 tcacctgcgg gttacaaaaa aaaataggtc acacatgtca aattagtgaa aacttggatt
241 cctattacac tcatgactt aaatttatta gttaaaatta aaccttatt

```

L6 ANSWER 94 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB184777 GenBank (R)

GenBank ACC. NO. (GBN): BB184777

GenBank VERSION (VER): BB184777.1 GI:8845348

CAS REGISTRY NO. (RN): 276633-09-1

SEQUENCE LENGTH (SQL): 215

MOLECULE TYPE (CI): mRNA; linear

DIVISION CODE (CI): Expressed sequence tag

DATE (DATE): 30 Jun 2000

DEFINITION (DEF): BB184777 RIKEN full-length enriched, adult male spinal cord Mus musculus cDNA clone A330015N04 3' similar to AF076619 Rattus norvegicus molecular adapter rGrb14 (***Grb14***) mRNA, mRNA sequence.

SOURCE: house mouse.

ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 87 a 32 c 38 g 58 t

COMMENT:

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URL:<http://genome.gsc.riken.go.jp/>

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome rtc.riken.go.jp>) for further details.

REFERENCE: 1 (bases 1 to 215)

AUTHOR (AU): Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.; Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.; Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.; Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.; Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.y.; Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.; Shibata,Y.; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.; Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.; Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a.; Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.; Yamanaka,I.; Yano,R.H.; Yasunishi,A.; Yokota,T.; Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.; Hayashizaki,Y.

TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al.)

JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key

Location

Qualifier

SEQUENCE (SEQ):

1 ttgtttcatt ccttacacca cagaagaaga acgatccaaa ggagtatgat tagagagaga
61 gagagagatc acaaggctga aaacaaatca tggtaaaaag aagatttcac ctgcgggta
121 caaaaaaaaaa taggtcacac attgcaaatt agtggaaact tggattccta ttacattcat
181 qactttaaat ttattagttt aaattaaacc ttatt

L6 ANSWER 95 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB173204 GenBank (R)
GenBank ACC. NO. (GBN): BB173204
GenBank VERSION (VER): BB173204.1 GI:8832287
CAS REGISTRY NO. (RN): 276506-98-0
SEQUENCE LENGTH (SQL): 282
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 29 Jun 2000
DEFINITION (DEF): BB173204 RIKEN full-length enriched, adult male
hypothalamus *Mus musculus* cDNA clone A230044K20 3'
similar to AF076619 *Rattus norvegicus* molecular adapter
rGrb14 (***Grb14***) mRNA. mRNA sequence.

SOURCE: house mouse.
ORGANISM (ORGN): *Mus musculus*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; *Mus*

NUCLEIC ACID COUNT (NA): 98 a 55 c 55 g 74 t

COMMENT:

ENT:
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
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URL: <http://genome.gsc.riken.go.jp/>

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome rtc.riken.go.jp>) for further details.

REFERENCE:

AUTHOR (AU):

1 (bases 1 to 282)

Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.; Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.; Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.; Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.; Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.y; Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.; Shibata,Y.; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.; Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.; Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a; Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.; Yamanaka,I.; Yano,R.H; Yasunishi,A.; Yokota,T.; Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.; Hayashizaki,Y.

TITLE (TI):

RIKEN Mouse ESTs (Konno,H., et al.)

JOURNAL (SO):

Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..282	/organism="Mus musculus" /db-xref="taxon:10090" /clone="A230044K20" /clone-lib="RIKEN full-length enriched, adult male hypothalamus" /sex="male" /tissue-type="hypothalamus" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: salI; site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTTTTTTTT TTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. "

SEQUENCE (SEQ):

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1 gctcaacagg gggtccttcc ttcccagctg aagcattact gtgcttaggat gcctgtttac
61 ccttaactctg tgtcactcgta tacactacag tagaagaagg atgcaaaggaa gaatgatcag
121 agagagagag agagatcaca agcctgaaaa caaatcatgg tgtaaagaag atttcacctg
181 cgggttacca aaaaaatag gtcacacattt ccaaatttagt gaaaacttgg attccttata
241 cactcatgac tttaaattttt ttagttaaaa tttaaacctta tt

```

L6 ANSWER 96 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB170892 GenBank (R)

GenBank ACC. NO. (GBN): BB170892

GenBank VERSION (VER): BB170892.1 GI:8829975

CAS REGISTRY NO. (RN): 276483-86-4

SEQUENCE LENGTH (SQL): 259

MOLECULE TYPE (CI): mRNA; linear

DIVISION CODE (CI): Expressed sequence tag

DATE (DATE): 29 Jun 2000

DEFINITION (DEF): BB170892 RIKEN full-length enriched, adult male
hypothalamus Mus musculus cDNA clone A230022B15 3'
similar to AF076619 Rattus norvegicus molecular adapter
rGrb14 (***Grb14***) mRNA, mRNA sequence.

SOURCE: house mouse.

ORGANISM (ORGN): Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 79 a 55 c 45 g 80 t

COMMENT:

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Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,

URL:<http://genome.gsc.riken.go.jp/>Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Y. and Hayashizaki,Y.Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)Please visit our web site (<http://genome rtc.riken.go.jp>) for
further details.

REFERENCE: 1 (bases 1 to 259)

AUTHOR (AU): Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.;
Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.;
Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.;
Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.;
Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.;
Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.;
Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.Y.;
Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.;
Shibata,Y.; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.;
Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.;
Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a.;
Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.;
Yamanaka,I.; Yano,R.H.; Yasunishi,A.; Yokota,T.;
Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.;
Hayashizaki,Y.

TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al.)

JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
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source 1..259 /organism="Mus musculus"
/db-xref="taxon:10090"
/clone="A230022B15"
/clone-lib="RIKEN full-length
enriched, adult male hypothalamus"
/sex="male"
/tissue-type="hypothalamus"
/dev-stage="adult"
/lab-host="DH10B"
/note="Site-1: Sali; site-2:
BamHI; cDNA library was prepared
and sequenced in Mouse Genome
Encyclopedia Project of Genome
Exploration Research Group in
Riken Genomic Sciences Center and
Genome Science Laboratory in
RIKEN. Division of Experimental
Animal Research in Riken
contributed to prepare mouse
tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAAGGATCCAAGAGCTTTTTTTT
TTTTTTTVN 3'], cDNA was prepared
by using trehalose
thermo-activated reverse
transcriptase and subsequently
enriched for full-length by
cap-trapper. cDNA went through one
round of normalization to Rot =
20.0 and subtraction to Rot =
459.0. Second strand cDNA was
prepared with the primer adapter
of sequence [5'
GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC
CCCCCCCCCCCC 3']. cDNA was cleaved
with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after
bulk excision from Lambda FLC I. "

SEQUENCE (SEQ):

1 cctgatatta tacacctaaa atgcatgcag acagatccct tacacagata ctgcacgtgt
61 ttttaagctc cagcacctat cctgaaatcc atggcttctt tcataccaaag gaacaggaa
121 agaattattg gaaaaaaagct tactttttt tcagaagatt tggcttataat ttttttacta
181 aaggcacatc caaggaacca tggcatttgc agctttcagc tgaattcagc actagtcacg
241 ttatatgtc actggcagg

L6 ANSWER 97 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB124451 GenBank (R)
GenBank ACC. NO. (GBN): BB124451
GenBank VERSION (VER): BB124451.1 GI:8777019
CAS REGISTRY NO. (RN): 275947-71-2
SEQUENCE LENGTH (SQL): 312
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 27 Jun 2000
DEFINITION (DEF): BB124451 RIKEN full-length enriched, adult male urinary
bladder *Mus musculus* cDNA clone 9530097N18 3' similar
to AF076619 *Rattus norvegicus* molecular adapter rGrb14
(***Grb14***) mRNA, mRNA sequence.

SOURCE: house mouse.
ORGANISM (ORGN): *Mus musculus*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; *Mus*

NUCLEIC ACID COUNT (NA): 108 a 60 c 60 g 84 t

COMMENT:

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Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/

Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome rtc. riken. go. jp>) for further details.

REFERENCE:

AUTHOR (AU):

1 (bases 1 to 312)
Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.; Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.; Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.; Hori, F.; Ishii, Y.; Ishikawa, J.; Ishikawa, T.; Itoh, M.; Izawa, M.; Kadota, K.; Kagawa, I.; Kai, C.; Kawai, J.; Kikuchi, N.; Kiyosawa, H.; Kojima, Y.; Kondo, S.; Koya, S.; Kurihara, C.; Kusakabe, M.; Matsuyama, T.; Miki, R.; Mizuno, Y.; Nakamura, M.; Oda, H.; Okazaki, Y.; Ono, T. y.; Owa, C.; Saito, H.; Sakai, C.; Sato, K.; Shibata, K.; Shibata, Y.; Shigemoto, Y.; Shinagawa, A.; Shiraki, T.; Sogabe, Y.; Sugahara, Y.; Suzuki, H.; Suzuki, H.; Tagawa, A.; Takahashi, F.; Tominaga, N.; Toya, T. a.; Tsunoda, Y.; Watahiki, A.; Watanabe, S.; Yamamura, T.; Yamanaka, I.; Yano, R. H.; Yasunishi, A.; Yokota, T.; Yoshida, K.; Yoshiki, A.; Yoshino, M.; Muramatsu, M.; Hayashizaki, Y.

TITLE (TI):

RIKEN Mouse ESTs (Konno, H., et al.)

JOURNAL (SO):

Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..312	/organism="Mus musculus" /db-xref="taxon:10090" /clone="9530097N18" /clone-lib="RIKEN full-length enriched, adult male urinary bladder" /sex="male" /tissue-type="urinary bladder" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: SalI; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTTTTTTTTT TTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 370.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after

SEQUENCE (SEQ):

1 gacttcatcc agcttgcgga gttttaccac ctctacaggg gggtccttcc ttgcaacctg
 61 aagcttact ttgcttaggaa ggcatttac cccaaactgtc tgcactcat tacactacag
 121 aagaagaagg atccatggaa gaatgattag agagagagag agagatcaca aggctgaaaa
 181 caaatcatgg tgaaaagaag atttcacctg cgggttacaa aaaaaaatag gtcacacatt
 241 gcttaattgt gaaaacttgg attccttatta cactcatgac tttaaatttta tttagttaaaa
 301 ttaaacctta tt

L6 ANSWER 98 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC):

BB115268 GenBank (R)

GenBank ACC. NO. (GBN): BB115268

GenBank VERSION (VER): BB115268.1 GI:8767836

CAS REGISTRY NO. (RN): 275855-88-4

SEQUENCE LENGTH (SQL): 235

MOLECULE TYPE (CI): mRNA; linear

DIVISION CODE (CI): Expressed sequence tag

DATE (DATE): 27 Jun 2000

DEFINITION (DEF): BB115268 RIKEN full-length enriched, adult male urinary bladder *Mus musculus* cDNA clone 9530049M14 3' similar to AF076619 *Rattus norvegicus* molecular adapter rGrb14 (***Grb14***) mRNA, mRNA sequence.

SOURCE: house mouse.

ORGANISM (ORGN): *Mus musculus*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; *Mus*

NUCLEIC ACID COUNT (NA): 89 a 39 c 45 g 62 t

COMMENT:

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URL:<http://genome.gsc.riken.go.jp/>

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki ,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome rtc.riken.go.jp>) for further details.

REFERENCE:

1 (bases 1 to 235)
 AUTHOR (AU): Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
 Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.;
 Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.;
 Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.;
 Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.;
 Kikuchi,N.; Kirosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.;
 Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.;
 Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.y.;
 Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.;
 Shibata,Y.; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.;
 Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.;
 Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a.;
 Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.;
 Yamanaka,I.; Yano,R.H.; Yasunishi,A.; Yokota,T.;
 Yoshida,K.; Yoshiki,A.; Yoshino,M..; Muramatsu,M.;
 Hayashizaki,Y.

TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al.)

JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..235	<p>/organism="Mus musculus" /db-xref="taxon:10090" /clone="9530049M14" /clone-lib="RIKEN full-length enriched, adult male urinary bladder" /sex="male" /tissue-type="urinary bladder" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: Sali; Site-2: BamHI; cDNA Library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTTTTTTT TTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 370.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."</p>

SEQUENCE (SEQ):

```

1 atggctgttt atccctactg cgtctcaactc gttacactac agaaggagaa ggattctaag
61 gagaatgatc agagagagag agagagatca caaggctgaa aacaaatcat ggtgaaaaga
121 agatttcacc tgccggttac caaaaaaaaaa taggtcacac attgcaaatt agtggaaaact
181 tggattcccta ttacactcat gactttaat ttatttagtta aaattaaacc ttatt

```

L6 ANSWER 99 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB114126 GenBank (R)
 GenBank ACC. NO. (GBN): BB114126
 GenBank VERSION (VER): BB114126.1 GI:8766694
 CAS REGISTRY NO. (RN): 275844-46-7
 SEQUENCE LENGTH (SQL): 316
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 27 Jun 2000
 DEFINITION (DEF): BB114126 RIKEN full-length enriched, adult male urinary
 bladder Mus musculus cDNA clone 9530044F23 3' similar
 to AF076619 Rattus norvegicus molecular adapter rGrb14
 (***Grb14***) mRNA, mRNA sequence.
 SOURCE: house mouse.
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus
 NUCLEIC ACID COUNT (NA): 110 a 67 c 55 g 84 t

COMMENT:

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Email: genome-res@gsc.riken.go.jp,
URL:<http://genome.gsc.riken.go.jp/>

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome rtc.riken.go.jp>) for further details.

REFERENCE:

AUTHOR (AU):

1 (bases 1 to 316)

Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.; Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.; Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.; Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.; Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.y; Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.; Shibata,Y.; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.; Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.; Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a; Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.; Yamanaka,I.; Yano,R.H.; Yasunishi,A.; Yokota,T.; Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.; Hayashizaki,Y.

TITLE (TI):

RIKEN Mouse ESTs (Konno,H., et al.)

JOURNAL (SO):

Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..316	/organism="Mus musculus" /db-xref="taxon:10090" /clone="9530044F23" /clone-lib="RIKEN full-length enriched, adult male urinary bladder" /sex="male" /tissue-type="urinary bladder" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: Sali; site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTTTTTTTT TTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 370.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCCCCC 3']. cDNA was cleaved

with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

SEQUENCE (SEQ):

1 ccacagacac tatccagcac gtcgattca ccagctccat aggggggtcc ttccttgcca
61 cctgaaacat tactttctt ggaagcctct ttacccaaac ttgtttcac tccttacact
121 acagaagaag aaggatccaa aggagaatga tcagagagag agagagagat cactaggctg
181 aaaacaaatc atggtaaaaa gaagattaa cctgcgggtt aaaaaaaaaa ataggtcaca
241 cattgcaaat tagtgaaaac ttggattcct attacactca tgactttaaa tttatttagtt
301 aaaattaaac cttatt

L6 ANSWER 100 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB108361 GenBank (R)
GenBank ACC. NO. (GBN): BB108361
GenBank VERSION (VER): BB108361.1 GI:8760929
CAS REGISTRY NO. (RN): 275745-24-9
SEQUENCE LENGTH (SQL): 249
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 27 Jun 2000
DEFINITION (DEF): BB108361 RIKEN full-length enriched, adult male urinary bladder *Mus musculus* cDNA clone 9530011B11 3' similar to AF076619 *Rattus norvegicus* molecular adapter rGrb14 (***Grb14***) mRNA, mRNA sequence.
SOURCE: house mouse.
ORGANISM (ORGN): *Mus musculus*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; *Mus*
NUCLEIC ACID COUNT (NA): 102 a 44 c 39 g 64 t

COMMENT:

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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:<http://genome.gsc.riken.go.jp/>
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki ,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (<http://genome rtc.riken.go.jp>) for further details.

REFERENCE: 1 (bases 1 to 249)

AUTHOR (AU): Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.; Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.; Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.; Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.; Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.y.; Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.; Shibata,Y.; Shigemoto,Y.; shinagawa,A.; Shiraki,T.; Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.; Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a.; Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.; Yamanaka,I.; Yano,R.H.; Yasunishi,A.; Yokota,T.; Yoshida,K.; Yoshiki,A.; Yoshino,M..; Muramatsu,M.; Hayashizaki,Y.

TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al.)

JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..249	<pre> /organism="Mus musculus" /db-xref="taxon:10090" /clone="9530011B11" /clone-lib="RIKEN full-length enriched, adult male urinary bladder" /sex="male" /tissue-type="urinary bladder" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: Sali; site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTTTTTTTT TTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 370.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTC CCCCCCCCCCC 3']. cDNA was cleaved with XbaI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I." </pre>

SEQUENCE (SEQ):

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1 acccttatc tgcaaggatg actatttacc caaactatct ctcactcatt acacaacaga
61 agaagaagga ttcaaaggag aatgattaga gagagagaga gatcacaagc ctgaaaacaa
121 atcatggta aaagaagatt tcacctgcgg gttacaaaaa aaaataggtc acacattcca
181 aattagtgaa aacttggatt cctattacac tcatgacttt aaatttatta gttaaaattt
241 aaccttatt

```

L6 ANSWER 101 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB070600 GenBank (R)
 GenBank ACC. NO. (GBN): BB070600
 GenBank VERSION (VER): BB070600.1 GI:8580598
 CAS REGISTRY NO. (RN): 273680-63-0
 SEQUENCE LENGTH (SQL): 270
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 25 Jun 2000
 DEFINITION (DEF): BB070600 RIKEN full-length enriched, 15 days embryo
 male testis Mus musculus cDNA clone 8030491011 3'
 similar to AF076619 Rattus norvegicus molecular adapter
 rGrb14 (***Grb14***) mRNA, mRNA sequence.
 SOURCE: house mouse.
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus
 NUCLEIC ACID COUNT (NA): 93 a 57 c 45 g 75 t
 COMMENT:
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,

URL: <http://genome.gsc.riken.go.jp/>

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome rtc.riken.go.jp>) for further details.

REFERENCE:

AUTHOR (AU):

1 (bases 1 to 270)

Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.; Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.; Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.; Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.; Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.y; Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.; Shibata,Y.; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.; Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.; Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a; Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.; Yamanaka,I., Yano,R.H; Yasunishi,A.; Yokota,T.; Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.; Hayashizaki,Y.

TITLE (TI):

RIKEN Mouse ESTs (Konno,H., et al.)

JOURNAL (SO):

Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..270	/organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="8030491011" /clone-lib="RIKEN full-length enriched, 15 days embryo male testis" /sex="male" /tissue-type="testis" /dev-stage="15 days embryo" /lab-host="DH10B" /note="Site-1: SalI; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTTTTTTTTT TTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rot = 185.0 Second strand cDNA was prepared with the primer adapter

of sequence [5'
GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC
CCCCCCCCCCCC 3']. cDNA was cloned
into the XbaI and BamHI sites.
Vector: a modified pBluescript
KS(+) after bulk excision from
Lambda FLC I. Cloning sites, 5'
end: SalI; 3' end: BamHI"

SEQUENCE (SEQ):

1 ctccttcctt ctttgctgca ccaatcctat gtttggatgc ctgcttaacc caactgtgt
61 tcactcataa cactacagca gtatggat ccaatggagg atgatttagag agagagag
121 agatcacaag cctgaaaca aatcatggtg aaaagaat ttcaccccg gcttacaaaa
181 aaaaatagct cacacattgc aaatttagtga aaacttggat tcctattaca ctcatgactt
241 taaaatttatt agttaaaaatt aaaccttatt

L6 ANSWER 102 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB045416 GenBank (R)
GenBank ACC. NO. (GBN): BB045416
GenBank VERSION (VER): BB045416.1 GI:8451802
CAS REGISTRY NO. (RN): 272392-50-4
SEQUENCE LENGTH (SQL): 323
MOLECULE TYPE (CI): mRNA; Linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 23 Jun 2000
DEFINITION (DEF): BB045416 RIKEN full-length enriched, 13 days embryo
male testis Mus musculus cDNA clone 6030495A12 3'
similar to AF076619 Rattus norvegicus molecular adapter
rGrb14 (***Grb14***) mRNA, mRNA sequence.
SOURCE: house mouse.
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 113 a 63 c 59 g 88 t

COMMENT:

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Email: genome-res@gsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
, N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
, Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (<http://genome rtc.riken.go.jp>) for
further details.

REFERENCE:

AUTHOR (AU): 1 (bases 1 to 323)
Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.;
Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.;
Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.;
Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.;
Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.;
Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.;
Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.y.;
Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.;
Shibata,Y.; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.;
Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.;
Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a.;
Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.;
Yamanaka,I.; Yano,R.H.; Yasunishi,A.; Yokota,T.;

Yoshida,K.; Yoshiki,A.; Yoshino,M.;
Muramatsu,M.;
Hayashizaki,Y.
TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al.)
JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..323	/organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="6030495A12" /clone-lib="RIKEN full-length enriched, 13 days embryo male testis" /sex="male" /tissue-type="testis" /dev-stage="13 days embryo" /lab-host="DH10B" /note="Site-1: SalI; site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTTTTTTTT TTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

SEQUENCE (SEQ):

1 attcccaagtt ctcagacctt atccagctcc ggattacacc acttcacagg gggttccttc
61 cttccaaact gaagcattat tgccttagga tggctgtta gccaaactct gtttcaatcg
121 ttacactaca gaagaagaag gatccaaagg agaatgatta gagagagaga gagagatcac
181 aaggctgtaa acaaattcatg gtggaaagaa gatttcacct gcgggttaca aaaaaaaaaata
241 ggtcacacat tgcaaattag tgaaaacttg gattcctatt acactcatga ctttaaattt
301 attagttaaa attaaacacctt att

L6 ANSWER 103 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB042697 GenBank (R)
GenBank ACC. NO. (GBN): BB042697
GenBank VERSION (VER): BB042697.1 GI:8449083
CAS REGISTRY NO. (RN): 272365-31-8
SEQUENCE LENGTH (SQL): 289
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 23 Jun 2000
DEFINITION (DEF): BB042697 RIKEN full-length enriched, 13 days embryo
male testis Mus musculus cDNA clone 6030465G02 3'
similar to AF076619 Rattus norvegicus molecular adapter
rGrb14 (***Grb14***) mRNA, mRNA sequence.
SOURCE: house mouse.
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 104 a 62 c 51 g 72 t

COMMENT:

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,

URL:<http://genome.gsc.riken.go.jp/>

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki ,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome rtc.riken.go.jp>) for further details.

REFERENCE:

AUTHOR (AU):

1 (bases 1 to 289)

Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.; Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.; Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.; Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.; Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.y.; Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.; Shibata,Y.; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.; Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.; Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a.; Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.; Yamanaka,I., Yano,R.H; Yasunishi,A.; Yokota,T.; Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.; Hayashizaki,Y.

TITLE (TI):

RIKEN Mouse ESTs (Konno,H., et al.)

JOURNAL (SO):

Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..289	/organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="6030465G02" /clone-lib="RIKEN full-length enriched, 13 days embryo male testis" /sex="male" /tissue-type="testis" /dev-stage="13 days embryo" /lab-host="DH10B" /note="Site-1: SalI; site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTTTTTTTT TTTTTTTVN 3'], cDNA was prepared

by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAAATCC CCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

SEQUENCE (SEQ):

1 tctaccacta cacacggggt ctttcccccc aaccaggcgc attactgtcc taggatcccc
61 gtttacccta actctgtgtc actcgttaca ccacagaaga agaaggatcc aaaggagaat
121 gatttagagag agagagagag atcacaaggc tgaatacaaa tcatgggtaa aagaagattt
181 cacctgcggg ttacaaaaaa aaaataggtc acacattgca aattagtgaa aacttggatt
241 cctattacac tcatgactt aaatttatta gttaaaatta aaccttatt

L6 ANSWER 104 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB037605 GenBank (R)
GenBank ACC. NO. (GBN): BB037605
GenBank VERSION (VER): BB037605.1 GI:8443991
CAS REGISTRY NO. (RN): 272314-39-3
SEQUENCE LENGTH (SQL): 237
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 23 Jun 2000
DEFINITION (DEF): BB037605 RIKEN full-length enriched, 13 days embryo forelimb Mus musculus cDNA clone 5930428012 3' similar to AF076619 Rattus norvegicus molecular adapter rGrb14 (***Grb14***) mRNA, mRNA sequence.
SOURCE: house mouse.
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 84 a 50 c 40 g 63 t
COMMENT:

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,

URL:<http://genome.gsc.riken.go.jp/>

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome rtc.riken.go.jp>) for further details.

REFERENCE: 1 (bases 1 to 237)

AUTHOR (AU): Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.; Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.;

Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.;
Kurihara,C.; Kusakabe,M., Matsuyama,T.; Miki,R.;
Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y., Ono,T.y;
Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.;
Shibata,Y., Shigemoto,Y.; Shinagawa,A.; Shiraki,T.;
Sogabe,Y.; Sugahara,Y., Suzuki,H., Suzuki,H.;
Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a;
Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.;
Yamanaka,I., Yano,R.H; Yasunishi,A.; Yokota,T.;
Yoshida,K.; Yoshiki,A.; Yoshino,M..; Muramatsu,M.;
Hayashizaki,Y.

TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al.)
JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..237	/organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="5930428012" /clone-lib="RIKEN full-length enriched, 13 days embryo forelimb" /sex="mixed" /tissue-type="forelimb" /dev-stage="13 days embryo" /lab-host="DH10B" /note="Site-1: SalI; site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTTTTTTTT TTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

SEQUENCE (SEQ):

1 ggattgctct tttcccaaac tgtacacctac tccttacacc acaggagcag aaggatcccc
61 cggagaatga ttagagagag agagagaaaat cacatggctg aaaacaaaatc ttggtaaaaa
121 ccagatttca cctccgggtt accaaaaaaaaa ataggtcaca ctttccaaat tagtggaaac
181 ttggatttcct attacactca tgactttaaa tttatttagtt aaaattaaac cttattg

L6 ANSWER 105 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AF155647 GenBank (R)
GenBank ACC. NO. (GBN): AF155647
GenBank VERSION (VER): AF155647.1 GI:7262856
CAS REGISTRY NO. (RN): 259713-78-5
SEQUENCE LENGTH (SQL): 1978
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Rodents
DATE (DATE): 19 Mar 2000
DEFINITION (DEF): Mus musculus adaptor protein ***GRB14*** (

SOURCE: ***Grb14***) mRNA, complete cds.
 ORGANISM (ORGN): house mouse.
 MUS musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus
 NUCLEIC ACID COUNT (NA): 559 a 491 c 492 g 436 t
 REFERENCE:
 AUTHOR (AU): Reilly, J.F.; Mickey, G.; Maher, P.A.
 TITLE (TI): Association of fibroblast growth factor receptor 1 with
 the adaptor protein ***Grb14*** . Characterization
 of a new receptor binding partner
 JOURNAL (SO): J. Biol. Chem., 275 (11), 7771-7778 (2000)
 OTHER SOURCE (OS): CA 132:330035
 REFERENCE:
 AUTHOR (AU): Reilly, J.F.; Mickey, G.; Maher, P.A.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (01-JUN-1999) Cell Biology, The Scripps
 Research Institute, 10550 N. Torrey Pines Rd., CAL-3,
 La Jolla, CA 92037, USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1978	/organism="Mus musculus" /db-xref="taxon:10090" /cell-line="NIH/3T3" /gene="Grb14"
5' UTR	1..122	
gene	1..1978	
CDS	123..1739	
3' UTR	1740..1978	

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1 gcccgcctgc caccgcacct gcaaggcgct cgctgcctgc aaccgcctcg ctctgctcgc
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 121 ccatgaccac gtcctgccaa gacggggcaga ggcgcgcggg cccgggcaggc gcccaggatt
 181 cggccgtggc agtgcagggtg tgccgcgtt cccaggccaa gggagacgc caggaccgg
 241 cgcagggtccc cggactgcac ggcgtgtccc cgcgcctccga tgcgaccctc cgccgtgcca
 301 tagacaggag aaaaatgaaa gatctggatg ttctggaaaa gccacccatt cccaaacccct
 361 ttccctgagct ctgcgtctc cgcgttacat ctgtgcgtc agcaggccctg tttcccaagg
 421 ccaattcaag gaagaagcag gtgattaaag tttacagcga ggtatgaaacc agcagagcat
 481 tagagggtgcc cagtgcacatc acagccccgag atgtttgcca gctgttgatc ctgaagaacc
 541 actatgtgga cgacaacagc tggacccttt ttgagcacct atctcacata ggttttagaaa
 601 gaaccgtaga ggaccacag ctgccaactg aagtgcgtc tcactggggg gtggagaag
 661 acaataagct gtatctttaga aagaattatg ccaaataatga attttttaag aacccaatgt
 721 atttctttcc agagcacatg gtgtctttt cagctgaaat gaatgggtgac agatcccata
 781 cacagatact gcagggtgtt ttaagctcca gcacgtatcc tggaaatccat ggcttcttac
 841 atgcaaagga acagggaaag aagtcttggg aaaaagctt cttttttctc agaagatctg
 901 gcttatattt ttctactaaa ggcacatcca aggaaccacg gcatttgacat cttttcagtg
 961 aattcagcac tagtcacgtt tataatgtcac tggcaggaaa aaaaaaaacac ggagcgccaa
1021 ctcccttatgg attctgccttta aagcctaaca aagcaggagg gccccgggac ctgaaaatgc
1081 tctgtgcaga agaagagcag agcaggacgt gctgggtgac cgccatccga ctgctgaagg

```

1141 atggcatgca gctgtatcag aattatatgc atccatacca aggtagaagc gcctgcaatt
1201 ctcagagcat gtcacccatg agaagcgtat cagagaattc cctagtagca atggacttct
1261 caggtagaaa gaggcagatc atagacaacc ccactgaagc gctttcggtt gctgttgagg
1321 aaggcctcgc gtggaggaaa aaaggctgtt tacgcctggg gaatcacgga agccccagtg
1381 cccccctccca gagctctgct gtgaacatgg ctctccatcg gtcccaacca tggtttacc
1441 acagaatttc cagagatgag gtcagcggc tgatcattcg gcaggggccct gtggatggag
1501 ttttcttggt acgggatagt cagagtaacc ccagaactt tttactgtca atgagtcatt
1561 gacaaaagat aaaacactat caaattatac ccgtagaaga tttatggtag ctgttccata
1621 ctctggatga tggccatagc aagttcacag acctcatcca gctgggtggag ttctaccagc
1681 tcaacagggg ggtccttcct tgcagctga agcattactg tgcttaggatg gctgtttagc
1741 caaactgtgt gtcactcggtt acactacaga agaagaagga tgcaaaaggag aatgattaga
1801 gagagagaga gagatcacaa ggctgaaaac aaatcatggt gaaaagaaga tttcacctgc
1861 gggttacaaa aaaaaatagg tcacacattg caaattatgtt aaaaacttggg ttccttattac
1921 actcatgact ttaaatttat tagttaaaat taaaccttat taaaaaaaaaaaaaaa

L6 ANSWER 106 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AV362938 GenBank (R)
GenBank ACC. NO. (GBN): AV362938
GenBank VERSION (VER): AV362938.1 GI:6410585
CAS REGISTRY NO. (RN): 249018-61-9
SEQUENCE LENGTH (SQL): 207
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 14 Nov 1999
DEFINITION (DEF): AV362938 RIKEN full-length enriched, 15 days embryo
male testis Mus musculus cDNA clone 8030405L12 3'
similar to AF076619 Rattus norvegicus molecular adapter
rGrb14 (***Grb14***) mRNA, mRNA sequence.
SOURCE: house mouse.
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 76 a 37 c 34 g 60 t
COMMENT:

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,

URL: <http://genome.gsc.riken.go.jp/>

Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
,Y.

Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)

Please visit our web site (<http://genome rtc.riken.go.jp>) for
further details.

REFERENCE: 1 (bases 1 to 207)

AUTHOR (AU): Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.;
Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.;
Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.;
Kai,C.?; Kawai,J.; Kikuchi,N.; Kojima,Y.; Koya,S.;
Kusakabe,M.; Matsuyama,T.; Miki,R.; Mizuno,Y.;
Nakamura,M.; Oda,H.; Okazaki,Y.; Owa,C.; Ozawa,Y.;
Saito,H.; Sano,M.; Sato,K.; Shibata,K.; Shibata,Y.;
Shigemoto,Y.; Shiraki,T.; Sogabe,Y.; Sugahara,Y.;
Suzuki,H.; Suzuki,H.; Takahashi,F.; Tateno,M.;
Tominaga,N.; Tsunoda,Y.; Watahiki,A.; Watanabe,S.;
Yamamura,T.; Yasunishi,A.; Yokota,T.; Yoshiki,A.;
Yoshino,M.; Muramatsu,M.; Hayashizaki,Y.

TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al. 1999)

JOURNAL (SO): Unpublished (1999)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..207	<pre> /organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="8030405L12" /clone-lib="RIKEN full-length enriched, 15 days embryo male testis" /sex="male" /tissue-type="testis" /dev-stage="15 days embryo" /lab-host="DH10B" /note="Site-1: SalI; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTTTTTTTT TTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rot = 185.0 Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI" </pre>

SEQUENCE (SEQ):

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1 attttttctc tacagcagga gaaggatccc aaggagaatg attagagaga gagagagaca
61 tcaccagcct gaaaacaaat tatgctgcac aggagattc acctccggct tactaaagaa
121 aatagttcac acattccaaa tttagtggaaa cttggattcc tattacaatc ttgactttaa
181 atttattagt taaaatttaa ccttatt

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L6 ANSWER 107 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AV355587 GenBank (R)
 GenBank ACC. NO. (GBN): AV355587
 GenBank VERSION (VER): AV355587.1 GI:6396644
 CAS REGISTRY NO. (RN): 248828-30-0
 SEQUENCE LENGTH (SQL): 231
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 12 Nov 1999
 DEFINITION (DEF): AV355587 RIKEN full-length enriched, adult male adrenal
 gland *Mus musculus* cDNA clone 7330413L18 3' similar to
 AF076619 *Rattus norvegicus* molecular adapter rGrb14 (***Grb14***) mRNA, mRNA sequence.

SOURCE: house mouse.
 ORGANISM (ORGN): *Mus musculus*
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; *Mus*

NUCLEIC ACID COUNT (NA): 93 a 32 c 36 g 70 t

COMMENT:

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Email: genome-res@gsc.riken.go.jp,

URL: <http://genome.gsc.riken.go.jp/>

Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
,Y.

Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)

Please visit our web site (<http://genome rtc.riken.go.jp>) for
further details.

REFERENCE:

AUTHOR (AU):

1 (bases 1 to 231)

Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.;
Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.;
Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.;
Kai,C.?; Kawai,J.; Kikuchi,N.; Kojima,Y.; Koya,S.;
Kusakabe,M.; Matsuyama,T.; Miki,R.; Mizuno,Y.;
Nakamura,M.; Oda,H.; Okazaki,Y.; Owa,C.; Ozawa,Y.;
Saito,H.; Sano,M.; Sato,K.; Shibata,K.; Shibata,Y.;
Shigemoto,Y.; Shiraki,T.; Sogabe,Y.; Sugahara,Y.;
Suzuki,H.; Suzuki,H.; Takahashi,F.; Tateno,M.;
Tominaga,N.; Tsunoda,Y.; Watahiki,A.; Watanabe,S.;
Yamamura,T.; Yasunishi,A.; Yokota,T.; Yoshiki,A.;
Yoshino,M.; Muramatsu,M.; Hayashizaki,Y.

TITLE (TI):

RIKEN Mouse ESTs (Konno,H., et al. 1999)

JOURNAL (SO):

Unpublished (1999)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..231	/organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="7330413L18" /clone-lib="RIKEN full-length enriched, adult male adrenal gland" /sex="male" /tissue-type="adrenal gland" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: SalI; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAAGGATCCAAGAGCTTTTTTTT TTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5'

GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC
CCCCCCCCCCCC 3']. cDNA was cloned
into the XbaI and BamHI sites.
Vector: a modified pBluescript
KS(+) after bulk excision from
Lambda FLC I. Cloning sites, 5'
end: SalI; 3' end: BamHI"

SEQUENCE (SEQ):

1 gcttttacc ctaattatct ttcaattttt atactacaga agaagaaggca tccaaaggag
61 aatgattaga gagagagaga gaaatcacaa ggctgaaaac aaattatggt gaaaagaaga
121 tttcacctgc gggttacaaa aaaaaatagt tcacacattg caaattatgtg aaaacttgg
181 ttccttattac attcatgact ttaaatttat tagtttaat taaaacttat t

L6 ANSWER 108 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AV335961 GenBank (R)
GenBank ACC. NO. (GBN): AV335961
GenBank VERSION (VER): AV335961.1 GI:6376013
CAS REGISTRY NO. (RN): 248628-93-5
SEQUENCE LENGTH (SQL): 193
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 11 Nov 1999
DEFINITION (DEF): AV335961 RIKEN full-length enriched, adult male medulla oblongata *Mus musculus* cDNA clone 6330578M15 3' similar to AF076619 *Rattus norvegicus* molecular adapter rGrb14 (***Grb14***) mRNA, mRNA sequence.
SOURCE: house mouse.
ORGANISM (ORGN): *Mus musculus*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; *Mus*
NUCLEIC ACID COUNT (NA): 73 a 32 c 35 g 52 t 1 others
COMMENT:

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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
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Email: genome-res@gsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>

Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
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Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)

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REFERENCE: 1 (bases 1 to 193)

AUTHOR (AU): Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.;
Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.;
Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.;
Kai,C.%; Kawai,J.; Kikuchi,N.; Kojima,Y.; Koya,S.;
Kusakabe,M.; Matsuyama,T.; Miki,R.; Mizuno,Y.;
Nakamura,M.; Oda,H.; Okazaki,Y.; Owa,C.; Ozawa,Y.;
Saito,H.; Sano,M.; Sato,K.; Shibata,K.; Shibata,Y.;
Shigemoto,Y.; Shiraki,T.; Sogabe,Y.; Sugahara,Y.;
Suzuki,H.; Suzuki,H.; Takahashi,F.; Tateno,M.;
Tominaga,N.; Tsunoda,Y.; Watahiki,A.; Watanabe,S.;
Yamamura,T.; Yasunishi,A.; Yokota,T.; Yoshiki,A.;
Yoshino,M.; Muramatsu,M.; Hayashizaki,Y.

TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al. 1999)

JOURNAL (SO): Unpublished (1999)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..193	<pre> /organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="6330578M15" /clone-lib="RIKEN full-length enriched, adult male medulla oblongata" /sex="male" /tissue-type="medulla oblongata" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: SalI; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTTTTTTTT TTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCCCCC 3']. cDNA was cloned into the XbaI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI" </pre>

SEQUENCE (SEQ):

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1 aagaaaagaag ggatcccaag gagcatgatt agagagagag aagagataac caggctgcac
61 accaatcatg gtgcaaagaa gaattttcac tttcggttaa ccnactaata gtcacacat
121 ttcaaattag tggaaacttg gattcctatt acattcatga ctttaaattt attagttaaa
181 attaaacctt att

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L6 ANSWER 109 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AV327707 GenBank (R)
 GenBank ACC. NO. (GBN): AV327707
 GenBank VERSION (VER): AV327707.1 GI:6367759
 CAS REGISTRY NO. (RN): 248487-17-4
 SEQUENCE LENGTH (SQL): 286
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 11 Nov 1999
 DEFINITION (DEF): AV327707 RIKEN full-length enriched, adult male medulla
 oblongata Mus musculus cDNA clone 6330436D10 3' similar
 to AF076619 Rattus norvegicus molecular adapter rGrb14
 (***Grb14***) mRNA, mRNA sequence.
 SOURCE: house mouse.
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus
 NUCLEIC ACID COUNT (NA): 105 a 52 c 53 g 76 t
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URL: <http://genome.gsc.riken.go.jp/>

Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
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Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)

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further details.

REFERENCE:
AUTHOR (AU): Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.;
Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.;
Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.;
Kai,C.?; Kawai,J.; Kikuchi,N.; Kojima,Y.; Koya,S.;
Kusakabe,M.; Matsuyama,T.; Miki,R.; Mizuno,Y.;
Nakamura,M.; Oda,H.; Okazaki,Y.; Owa,C.; Ozawa,Y.;
Saito,H.; Sano,M.; Sato,K.; Shibata,K.; Shibata,Y.;
Shigemoto,Y.; Shiraki,T.; Sogabe,Y.; Sugahara,Y.;
Suzuki,H.; Suzuki,H.; Takahashi,F.; Tateno,M.;
Tominaga,N.; Tsunoda,Y.; Watahiki,A.; Watanabe,S.;
Yamamura,T.; Yasunishi,A.; Yokota,T.; Yoshiki,A.;
Yoshino,M.; Muramatsu,M.; Hayashizaki,Y.
TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al. 1999)
JOURNAL (SO): Unpublished (1999)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..286	/organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="6330436D10" /clone-lib="RIKEN full-length enriched, adult male medulla oblongata" /sex="male" /tissue-type="medulla oblongata" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: Sali; site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAAGGATCCAAGAGCTTTTTTTTT TTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5'

GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC
CCCCCCCCCCCC 3']. cDNA was cloned
into the XhoI and BamHI sites.
Vector: a modified pBluescript
KS(+) after bulk excision from
Lambda FLC I. Cloning sites, 5'
end: SalI; 3' end: BamHI"

SEQUENCE (SEQ):

1 gcaccagtca tcagggcctc cttcctccca aactgaagca ttattatgct aggatggctg
61 ttcagccata ctcttctcat tcttatacta cagaagaaga aggatgccaa aggagaatga
121 ttagagagag agagagagat cacaaggctg aaaacaaatc atggtaaaaa gaagattca
181 cctgcgggtt aaaaaaaaaa ataggtcaca cattgcaa at tagtggaaac ttggattcct
241 attacattca tgactttaaa tttattatgaaa aaaaattaaac cttatt

L6 ANSWER 110 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AV321727 GenBank (R)
GenBank ACC. NO. (GBN): AV321727
GenBank VERSION (VER): AV321727.1 GI:6291562
CAS REGISTRY NO. (RN): 247815-00-5
SEQUENCE LENGTH (SQL): 253
MOLECULE TYPE (CI): mRNA; Linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 9 Nov 1999
DEFINITION (DEF): AV321727 RIKEN full-length enriched, 13 days embryo
male testis Mus musculus cDNA clone 6030436014 3'
similar to AF076619 Rattus norvegicus molecular adapter
rGrb14 (***Grb14***) mRNA, mRNA sequence.
SOURCE: house mouse.
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 84 a 46 c 45 g 78 t
COMMENT:

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
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polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)

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further details.

REFERENCE: 1 (bases 1 to 253)

AUTHOR (AU): Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.;
Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.;
Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.;
Kai,C.?; Kawai,J.; Kikuchi,N.; Kojima,Y.; Koya,S.;
Kusakabe,M.; Matsuyama,T.; Miki,R.; Mizuno,Y.;
Nakamura,M.; Oda,H.; Okazaki,Y.; Owa,C.; Ozawa,Y.;
Saito,H.; Sano,M.; Sato,K.; Shibata,K.; Shibata,Y.;
Shigemoto,Y.; Shiraki,T.; Sogabe,Y.; Sugahara,Y.;
Suzuki,H.; Suzuki,H.; Takahashi,F.; Tateno,M.;
Tominaga,N.; Tsunoda,Y.; Watahiki,A.; Watanabe,S.;
Yamamura,T.; Yasunishi,A.; Yokota,T.; Yoshiki,A.;
Yoshino,M.; Muramatsu,M.; Hayashizaki,Y.

TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al. 1999)

JOURNAL (SO): Unpublished (1999)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..253	<p>/organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="6030436014" /clone-lib="RIKEN full-length enriched, 13 days embryo male testis" /sex="male" /tissue-type="testis" /dev-stage="13 days embryo" /lab-host="DH10B" /note="Site-1: SalI; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTTTTTTTT TTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."</p>

SEQUENCE (SEQ):

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1 gcagccttac tttttttttt cccaaactct cttttactcc tttatctaca
61 gtagaaggcg gttcaagcg agaatgatta gagagtgaga gtgagattac caggctgata
121 acaattcatg gtgaaaagaa gatttcaccc gcgggttaca aaaaaaaaaata ggtcacat
181 tgcaaattag tgaaaaacttg gattcctatt acattcatga ctttaaattt attagttaaa
241 attaaacctt att

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L6 ANSWER 111 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AV259119 GenBank (R)
GenBank ACC. NO. (GBN): AV259119
GenBank VERSION (VER): AV259119.1 GI:6246578
CAS REGISTRY NO. (RN): 246989-25-3
SEQUENCE LENGTH (SQL): 230
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 4 Nov 1999
DEFINITION (DEF): AV259119 RIKEN full-length enriched, adult male testis
(DH10B) Mus musculus cDNA clone 4930403H14 3' similar
to AF076619 Rattus norvegicus molecular adapter rGrb14
(***Grb14***) mRNA, mRNA sequence.
SOURCE: house mouse.
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 103 a 27 c 34 g 66 t
COMMENT:
Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
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Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)

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REFERENCE:

AUTHOR (AU):

1 (bases 1 to 230)
Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.;
Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.;
Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.;
Kai,C.?; Kawai,J.; Kikuchi,N.; Kojima,Y.; Koya,S.;
Kusakabe,M.; Matsuyama,T.; Miki,R.; Mizuno,Y.;
Nakamura,M.; Oda,H.; Okazaki,Y.; Owa,C.; Ozawa,Y.;
Saito,H.; Sano,M.; Sato,K.; Shibata,K.; Shibata,Y.;
Shigemoto,Y.; Shiraki,T.; Sogabe,Y.; Sugahara,Y.;
Suzuki,H.; Suzuki,H.; Takahashi,F.; Tateno,M.;
Tominaga,N.; Tsunoda,Y.; Watahiki,A.; Watanabe,S.;
Yamamura,T.; Yasunishi,A.; Yokota,T.; Yoshiki,A.;
Yoshino,M.; Muramatsu,M.; Hayashizaki,Y.
RIKEN Mouse ESTs (Konno,H., et al. 1999)

TITLE (TI):

JOURNAL (SO):

Unpublished (1999)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..230	/organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="4930403H14" /clone-lib="RIKEN full-length enriched, adult male testis (DH10B)" /sex="male" /tissue-type="testis" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: salI; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGGATCCAAGAGCTTTTTTT TTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTGAGTTAATTAAATTAATCC

cccccccccccc 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

SEQUENCE (SEQ):

1 atgttcttat ctaaaacttct taattnaata cactaaagaa gaagaatgaa acaaagaaga
61 aagatcagag agagagagaa atattacaag gttgaaaaca aatcttgggt aaaagaagat
121 ttaacctgcg gtttacaaaaaaa aaaaatagtt cacacattgc aaattagtga aaacttggat
181 tcctattaca atcatgactt taaatttt agttaaaatt aaaccttatt

L6 ANSWER 112 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AF190121 GenBank (R)
 GenBank ACC. NO. (GBN): AF190121
 GenBank VERSION (VER): AF190121.1 GI:6018121
 CAS REGISTRY NO. (RN): 244113-77-7
 SEQUENCE LENGTH (SQL): 2052
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Rodents
 DATE (DATE): 22 Nov 2000
 DEFINITION (DEF): *Rattus norvegicus* growth factor receptor binding protein GRB7 (Grb7) mRNA, complete cds.
 SOURCE: Norway rat.
 ORGANISM (ORGN): *Rattus norvegicus*
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; *Rattus*
 NUCLEIC ACID COUNT (NA): 440 a 602 c 548 g 462 t
 REFERENCE:
 AUTHOR (AU): Kasus-Jacobi,A.; Perdereau,D.; Auzan,C.; Clauser,E.;
 Van Obberghen,E.; Mauvais-Jarvis,F.; Girard,J.;
 Burnol,A.F.
 TITLE (TI): Identification of the rat adapter ***Grb14*** as an inhibitor of insulin actions
 JOURNAL (SO): J. Biol. Chem., 273 (40), 26026-26035 (1998)
 OTHER SOURCE (OS): CA 130:20710
 REFERENCE:
 AUTHOR (AU): Kasus-Jacobi,A.; Bereziat,V.; Perdereau,D.; Girard,J.;
 Burnol,A.F.
 TITLE (TI): Evidence for an interaction between the insulin receptor and Grb7. A role for two of its binding domains, PIR and SH2
 JOURNAL (SO): Oncogene, 19 (16), 2052-2059 (2000)
 OTHER SOURCE (OS): CA 133:69252
 REFERENCE:
 AUTHOR (AU): Burnol,A.F.; Perdereau,D.; Kasus-Jacobi,A.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (27-SEP-1999) UPR 1524, CNRS, 9 rue Jules Hetzel, Meudon 92190, France

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..2052	/organism="Rattus norvegicus" /db-xref="taxon:10116" /tissue-type="liver"
gene	1..2052	/gene="Grb7"
CDS	50..1657	/gene="Grb7" /note="molecular adapter" /codon-start=1 /product="growth factor receptor binding protein GRB7" /protein-id="AAF01776.1" /db-xref="GI:6018122" /translation="MELDLSPSHLSSSPEDVCPT PGTPPETPPPPDNPPPGDVRSQP LPIPSSRKLREEEFQATSLPSIPNPFPPELCSPPS QKPILGSSGARGLLPRDSSRLCV VKVYSEDGACRSVEAAGATARHCEMLVQRAHA LSDENWGLVECHPYLALERGLEDH ESVVEVQEAWPVGGDSRFIFRKNAKYELFKSPP HTLFPEKVMSSCLDTPTGISHEDL IQNFLNAGSFPEIQGFLQLRGSGRGSGRKLWKR"

FCFLRRSGLYYSTKGTSKDPRHLQ
 YVADINESNVYVVTQGRKLYGIPDFGFCVKPNK
 LRNGHKGLHIFCSEDEQSRTCWL
 AFRLFKYGVQLYKNYQQAQSRHRLSLSYLGSPPLR
 SVSDNTLVAMDFTSGHAGRVIENPQ
 EALSAATEEEAQAWRKKTNHRLSLPTPCSGLSLSA
 AIHRTQPWFHGRISREESQRLIGQ
 QGLVDGVFLVRESQRNPQGFVLSLCHLQKVKHYL
 ILPSEDEGCLYFSMDDGQTRFTDL
 LQLVEFHQLNRGILPCLLRHCCARVAL"

SEQUENCE (SEQ):

1 cttgggtcc cggtgtcccg ctccctctgc tggagttcct ccaggtgccca tggacttgga
 61 tctgagcccg tctcatctca gcagctcccc agaagatgtg tgcccaactc ctgggacccc
 121 tcccgagact cctccgcccc cgataaccc tccgcccggc gatgtgaagc ggtctcagcc
 181 tttgcccattc ccaagttagca gaaaacttcg agaagaggag tttcaggcaa cctctctacc
 241 ctccatcccccc aacccttcc ccgagctctg cagcccacct tcacagaaac ccattcttgg
 301 tgggtccctcc ggtgcttaggg ggttgcctcc tcgagactcc agccgcctc gtgtggtgaa
 361 ggtgtacagt gaagatggag cctgcccggc tgtggaaagtgc gcccggcggc cgacggctcg
 421 ccatgtgtgt gagatgtctgg tgtagcggc tcacgcccggc agcgtgaga actggggcct
 481 ggtggagtgc cacccttatt tggctcttggc gcccgggtttt gaggaccatg agtctgtgg
 541 agaagtgcag gaggccttggc ctgtgggtgg agacagccgc ttcatcttcc gtaaaaactt
 601 cgccaagttttaaacttca agacccctcc gcacaccctt ttcccagaaa agatggtttc
 661 cagctgtctgg gatacaccggc cggcatatccatgaaac ccatgaaagac ctcatccaga acttcctgaa
 721 tgctggcagc ttccctgaga tccagggtt cctgcagctt cggggatcag gcccgggggtc
 781 aggtcgaaag ctttggaaac gattcttctg cttcctgcgt cggctctggcc tctattactc
 841 gaccaagggc acctctaagg acccgagaca cctacatgtc gtggcagata taaatgagtc
 901 caatgtgtat gtggtgaccgc agggccgaa gctgtatggg ataccacgg acttcggctt
 961 ttgtgtcaag cccacaacgc ttccaaatgg ccacaagggg ctccacatct tctgcagcga
 1021 ggatgagcag agtcggactt gctggctgtc cgccttccgg ctcttcaagt acggggtaca
 1081 gctatataag aattatcagc aggcccagtc tcgtcacctg cgcttacatcg atttggggtc
 1141 tccacccttgg aggagtgtct cagataatac cctggggggc atggacttct ctggccatgc
 1201 tgggcgtgtc attgagaacc cccaggaagc tctgagtgct gcccacagagg aagccaggc
 1261 ctggaggaag aagacaaacc accgtctcag cctgcccacc cctgcgtccgc gcctgagcct
 1321 cagtgcagct atccatcgca cccagccctg gtttcatggc cgaatctccc gggagagag
 1381 ccagcggcta attggacagc agggccctggc ggtatggta ttccctggtcc gggagagcca
 1441 gcggaaaccca caggccttcg ttctgtctct gtgcacatcg cagaaagtca aacattatct
 1501 catcttgcca agcgaagatg aaggctgcct ttacttcagc atggatgacg gccagacccg
 1561 tttcacagac ctgctgcagc tgggtggatt ccaccagctg aaccggggca tcctgcccctg
 1621 cttgctgcgc cactgctgtc cccgtgtggc cctctgaggc cacacaagct gttacagcca
 1681 tggggctgtc tatcgccctt ctgctccgtt cagtggactc ggtgcagatg ggtggatga
 1741 taaacagatg aagagctccc cccacttttcc tcccactttt ttttttacc tccctcagg
 1801 aatgaaacat ccccccagccc tggtagac tggtagggca tgaaaggca ttatgagagg agtaggggca
 1861 tcctctcccc ttggtagac tggtagggca tgaaaggca ttatgagagg agtaggggca
 1921 gccccgggtgg tctcatggcc caccacact ctgtacagac tgagaggcca gttgatctgc
 1981 tctgttttat accagtgata ataaagatta tttttgata caaaaaaaaaaaaaaaa
 2041 aaaaaaaaaaa aa

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LOCUS (LOC): AI928176 GenBank (R)
 GenBank ACC. NO. (GBN): AI928176
 GenBank VERSION (VER): AI928176.1 GI:5664140
 CAS REGISTRY NO. (RN): 241373-88-6
 SEQUENCE LENGTH (SQL): 319
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 8 Mar 2000
 DEFINITION (DEF): wo95a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
 IMAGE:2463064 3' similar to TR:Q14449 Q14449
 GRB14 . ;, mRNA sequence.

SOURCE: human.
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo

NUCLEIC ACID COUNT (NA): 90 a 54 c 48 g 127 t

COMMENT:

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 399 Std Error: 0.00

Seq primer: -40UP from Gibco.

REFERENCE: 1 (bases 1 to 319)
AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..319	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:2463064" /clone-lib="NCI-CGAP-Kid11" /lab-host="DH10B" /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP-Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). subtraction by Bento Soares and M. Fatima Bonaldo. "

SEQUENCE (SEQ):

1 ttcctaagg ttaatttaa ctaatgaatt ttaaatgatg aatgtaaagt caatccaagt
61 ctttgcttat ttgcaatgca caaactattt ttttctaact tgcaggtgaa atacattctt
121 ttccatcatgt aatgtttcg cccttattta tggtctttt ttattttct tgagtccctt
181 tccttcaata gtttaataag tcacttctgg cttgtctaga gagcaatcct agcacaataa
241 tgtttcaact tgcaaggaag aacgcctta ttgagttgat agaactccac cagctgtatt
301 agatctgtaa atcttgtt

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LOCUS (LOC): AI870172 GenBank (R)
GenBank ACC. NO. (GBN): AI870172
GenBank VERSION (VER): AI870172.1 GI:5544140
CAS REGISTRY NO. (RN): 390159-63-4
SEQUENCE LENGTH (SQL): 745
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 7 Mar 2000
DEFINITION (DEF): w15e05.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone
IMAGE:2424992 3' similar to TR:Q14449 Q14449
GRB14 . ;, mRNA sequence.

SOURCE: human.
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 189 a 157 c 145 g 249 t 5 others

COMMENT:

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1767 Std Error: 0.00

Seq primer: -40UP from Gibco
High quality sequence stop: 414.
REFERENCE: 1 (bases 1 to 745)
AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..745	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:2424992" /clone-lib="NCI-CGAP-Ut1" /tissue-type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors" /lab-host="DH10B" /note="Organ: uterus; Vector: pCMV-SPORT6; Site-1: SalI; Site-2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

SEQUENCE (SEQ):

1 tcctaagggtt taattttaac taatgaattt taaaatgatga atgtaaaagtc aatccaagtc
61 tttgcttatt tgcaatgcac aaactatttt tttgttaactt gcaggtgaaa tacattcttt
121 tcacatggta atgtttcgc ctttattttt ggtctttat tatttttctt gagtcctttt
181 ccttcaatag tttaaataag tcaccttctg ggctgtcta gagagcaatc ctagcacaat
241 aatgtttcaa ctgcaagga agaacgcctt tattgagttt atagaactcc accagctgt
301 ttagatctgt aaatcttgc tgccatcat ccagtgtgtg gaacattca cccgtcatctt
361 ctactggat aatttggaaag tgctttat tttgtccatg actcattgac agtacgaaag
421 ttttgggggtt actctgacta tcccgatcca agaaaactcc atccacaatg cttgtctgaa
481 taatcaatcg ctgagccctca tctctagaaa ttttgggtt aaaccatggc tgggaccgg
541 ggatagccat gtntgtggca gagctctgtg aagagcagt gggctaccgt gagtgc
601 gctaaacat cttttttnc tccaagcgag tccctttca accgcaactg aaaggggctt
661 ccgtgggatn ttcttaatact ctgctttcc tgccctgaga agtcattgct accaggaaa
721 tctctgtnta cctcctcata ggtga

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LOCUS (LOC): AI767914 GenBank (R)
GenBank ACC. NO. (GBN): AI767914
GenBank VERSION (VER): AI767914.1 GI:5234435
CAS REGISTRY NO. (RN): 236629-01-9
SEQUENCE LENGTH (SQL): 429
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 21 Dec 1999
DEFINITION (DEF): wi99c10.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone
IMAGE:2401458 3' similar to TR:Q14449 Q14449
GRB14 . ;, mRNA sequence.

SOURCE: human.
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 112 a 74 c 74 g 168 t 1 others

COMMENT:

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 925 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 260.

REFERENCE: 1 (bases 1 to 429)

AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE (TI): National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..429	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:2401458" /clone-lib="NCI-CGAP-Kid12" /tissue-type="2 pooled tumors (clear cell type)" /lab-host="DH10B" /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP-Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1323912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo. "

SEQUENCE (SEQ):

1 ttttcctaag gtttaatttt aactaatgaa ttttaaatga tgaatgtaaa gtcaatccaa
61 gtctttgctt atttgcaatg cacaactat ttttttgtaa cttgcaggtg aaatacattc
121 ttttcacatg ataatgtttt cgccttatt tatggctttt tattatttt cttgagtcct
181 tttccttcaa tagttaata agtcacttct ggctgtcta gagagcaatc ctagcacaat
241 aatgttcaa cttgcaagga agaacgcctt tattgagttt atagaactcc accagcttt
301 ttagatctgt aattttgggg tggccatatac caggtgtgtg gaacatttca ccgtcatctt
361 ctactggat aattggaaaa gtgctttatt ntttgtcca tgactcttgg accgtaccaa
421 agttttggg

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LOCUS (LOC): AI760945 GenBank (R)
GenBank ACC. NO. (GBN): AI760945
GenBank VERSION (VER): AI760945.1 GI:5176612
CAS REGISTRY NO. (RN): 236076-02-1
SEQUENCE LENGTH (SQL): 312
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 21 Dec 1999
DEFINITION (DEF): wi70e05.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone
IMAGE:2398688 3' similar to TR:Q14449 Q14449
GRB14 . ;, mRNA sequence.

SOURCE:

ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 90 a 54 c 46 g 122 t

COMMENT:

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 403 Std Error: 0.00

Seq primer: -40UP from Gibco.

REFERENCE: 1 (bases 1 to 312)

AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..312	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:2398688" /clone-lib="NCI-CGAP-Kid12" /tissue-type="2 pooled tumors (clear cell type)" /lab-host="DH10B" /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP-Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1323912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo. "

SEQUENCE (SEQ):

1 tttcctaagg tttaatttta actaatgaat tttaaatgat gaatgtaaag tcaatccaag
61 tctttgctta ttgcataatgc acaaactatt tttttgttaac ttgcaggtga aatacattct
121 tttcacatga taacgtttc gccttattt atggctttt attattttc ttgagtcctt
181 ttccttcaat agtttaataa gtcacttctg gcttgcctag agagcaatcc tagcacaata
241 atgtttcaac ttgcaaggaa gaacgcctt attgagttga tagaactcca ccagctgtat
301 tagatctgta aa

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LOCUS (LOC): AI695260 GenBank (R)
GenBank ACC. NO. (GBN): AI695260
GenBank VERSION (VER): AI695260.1 GI:4983160
CAS REGISTRY NO. (RN): 233989-40-7
SEQUENCE LENGTH (SQL): 408
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 16 Dec 1999
DEFINITION (DEF): wa02b08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
IMAGE:2296887 3' similar to TR:Q14449 Q14449
GRB14 . ;, mRNA sequence.

SOURCE: human.
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 112 a 82 c 62 g 152 t

COMMENT:

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 848 Std Error: 0.00

Seq. primer: -40UP from Gibco

High quality sequence stop: 396.

REFERENCE: 1 (bases 1 to 408)

AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..408	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:2296887" /clone-lib="NCI-CGAP-Kid11" /lab-host="DH10B" /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I; site-2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP-Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "

SEQUENCE (SEQ):

1 tcctaagggt taattttaac taatgaattt taaaatgatga atgtaaagtc aatccaagtc
61 ttgcattttt tgcaatgcac aaactatttt tttgttaactt gcagggtgaaa tacattcttt
121 tcacatgata atgttttcgc ctttattttt ggtctttat tatttttctt gagtcctttt
181 ccttcaatag tttataatagt cacttctggc ttgtcttagag agcaatccta gcacaataat
241 gtttcaactt gcaaggaaga acgcccttat tgagttgata gaactccacc agctgttatta
301 gatctgtaaa tcttgtgtgg ccatcatccca gtgtgtggaa catttcaccg tcattttctt
361 cccatccaca agtccttgct gaataatcaa tcgctgagcc tcatttttta

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LOCUS (LOC): AI671320 GenBank (R)
GenBank ACC. NO. (GBN): AI671320
GenBank VERSION (VER): AI671320.1 GI:4851051
CAS REGISTRY NO. (RN): 232699-27-3
SEQUENCE LENGTH (SQL): 497
MOLECULE TYPE (CI): mRNA; Linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 17 Dec 1999
DEFINITION (DEF): wc29a02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
IMAGE:2316554 3' similar to TR:Q14449 Q14449
GRB14 . ;, mRNA sequence.

SOURCE: human.
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 144 a 100 c 87 g 164 t 2 others

COMMENT:

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 795 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 372.

REFERENCE: 1 (bases 1 to 497)

AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE (TI): National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..497	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:2316554" /clone-lib="NCI-CGAP-Kid11" /lab-host="DH10B" /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP-Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "

SEQUENCE (SEQ):

1 gcctgccagt gacacataaa tatcaattt gccaaattcg ctaaaaaactg caaatgccgc
61 ggttcctttg atgttccttt agtagaaaaa tataaaccag atcttcttag aaaaaagtaa
121 atttttttcc aagacttctt tccctgttct ttgcgtatgt aaaaaaccatg aatttcagga
181 tatgtgcttg aactcagaaa catctgcaaa atctgtgtgg gggatatttc accattgggt
241 tcagttgcaa aagataccat atgctctggaa aaaaaataca ttgggttttt aaagaactca
301 tatttggcat aattttttctt aaagtatagt ttgttttctt cttctatccc ccagttggat
361 agcacttcaa tcaccagttc gtggcttctt attgttcttt ctacacctat gtgaggcagg
421 tgctcanaaa gggtccagct gtggtcatca atgtaatgtat tcttcaggat caacagctga
481 ncaacatctc gagccgt

L6 ANSWER 119 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI624682 GenBank (R)
GenBank ACC. NO. (GBN): AI624682
GenBank VERSION (VER): AI624682.1 GI:4649613
CAS REGISTRY NO. (RN): 230649-94-2
SEQUENCE LENGTH (SQL): 533
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 14 Dec 1999
DEFINITION (DEF): ts43e12.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone
IMAGE:2231374 3' similar to TR:Q14449 Q14449
GRB14 . ;, mRNA sequence.

SOURCE: human.
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 144 a 104 c 91 g 193 t 1 others

COMMENT:

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1696 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 401
POLYA=No.

REFERENCE:
 AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
 Project (CGAP), Tumor Gene Index
 JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..533	<code>/organism="Homo sapiens"</code> <code>/db-xref="taxon:9606"</code> <code>/clone="IMAGE:2231374"</code> <code>/clone-lib="NCI-CGAP-Ut1"</code> <code>/tissue-type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors"</code> <code>/lab-host="DH10B"</code> <code>/note="Organ: uterus; Vector: pCMV-SPORT6; Site-1: SalI; Site-2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"</code>

SEQUENCE (SEQ):

```

1 tcctaagggtt taattttaac taatgaattt taaaatgatga atgtaaaagtc aatccaagtc
 61 tttgcttatt tgcaatgcac aaactatttt tttgtaactt gcaggtgaaa tacattcttt
121 tcacatggta atgtttcgc ccttattttt ggtcttttat tattttctt gagtcctttt
181 ccttcaatacg ttaataaagt cacttctggc ttgtcttagag agcaatccta gcacaataat
241 gtttcaactt gcaaggaga agcgccttat tgagttgata gaactccacc agctgtatta
301 gatctgtaaa tcttgtgtgg ccatcatcca gtgtgtggaa catttcaccc tcattttcta
361 ctggtataat ttgaaagtgc tttatttttt gtccatgact cattgacagt acgaaagttt
421 tggggttact ctgactatcc cgtaccaaga aaactccatc cacaagtcct tgctgaataaa
481 tcaatcgctg agcctcatct ctagaaatnt tgtgtgaacc atggctggga ccg

```

L6 ANSWER 120 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI610228 GenBank (R)
 GenBank ACC. NO. (GBN): AI610228
 GenBank VERSION (VER): AI610228.1 GI:4619395
 CAS REGISTRY NO. (RN): 390132-63-5
 SEQUENCE LENGTH (SQL): 701
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 13 May 1999
 DEFINITION (DEF): tp15g09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone
 IMAGE:2187904 3' similar to TR:Q14449 Q14449
 GRB14 . ;, mRNA sequence.
 SOURCE: human.
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo

NUCLEIC ACID COUNT (NA): 179 a 144 c 132 g 242 t 4 others

COMMENT:

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 803 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 406

POLYA=No.

REFERENCE:
 AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
 Project (CGAP), Tumor Gene Index
 JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..701	/organism="Homo sapiens" /clone="IMAGE:2187904" /clone-lib="NCI-CGAP-Gas4" /tissue-type="poorly differentiated adenocarcinoma with signet ring cell features" /lab-host="DH10B" /note="Organ: stomach; Vector: pCMV-SPORT6; Site-1: SalI; Site-2: NotI; Cloned unidirectionally. Primer: oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"

SEQUENCE (SEQ):

```

1 ttcttaagggtt taatttttaac taatgaattt taaatgatga atgtaaagtc aatccaaagtc
61 tttgcttatt tgcaatgcac aaactatttt tttgttaactt gcaggtgaaa tacattctt
121 tcacatggta atgttttcgc ctttatattt ggtctttat tattttctt gagtccttt
181 ccttcaatag tttataaagt cacttctggc ttgtcttagag agcaatccctt gcacaataat
241 gttcaactt gcaaggaaaga acggcccttat tgagttgata gaactccacc agctgttata
301 gatctgtaaa tcttgggtgg ccatcatcca gtgtgtggaa catttcaccg tcattttctt
361 ctgttataat ttgaaatgtc tcttattttt gtccatgact cattgacagt acgaaagttt
421 tgggttact ctgactatcc cgtacccaaa aactccatcc acaagtccctt gctgaataat
481 caatcgctga gcctcatctc tagaaatttt gtggtaaacatggctggg accggtgat
541 agccatgttt gtggcagagc tctgtgaaga gcagtggngc taccgtgagt gcccagccgt
601 aaacatcctt ttttnccttcc agcgagtccct tcttcaaccg caactgaaag ggcttcagnn
661 ggattttcta taactctgct tttctggctt gagaagtccat

```

L6 ANSWER 121 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI609572 GenBank (R)
GenBank ACC. NO. (GBN): AI609572
GenBank VERSION (VER): AI609572.1 GI:4618739
CAS REGISTRY NO. (RN): 230319-99-0
SEQUENCE LENGTH (SQL): 368
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 14 May 1999
DEFINITION (DEF): tw28a08.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone
IMAGE:2260982 3' similar to TR:Q14449 Q14449
GRB14 . ;, mRNA sequence.
SOURCE: human.
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 100 a 59 c 57 g 151 t 1 others

COMMENT:

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 318 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 324
POLYA=No.

REFERENCE:
AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..368	/organism="Homo sapiens" /db-xref="taxon:9606"

/clone="IMAGE:2260982"
 /clone-lib="NCI-CGAP-Ov35"
 /tissue-type="tumor, 5 pooled (see
 description)"
 /lab-host="DH10B"
 /note="Organ: ovary; Vector:
 pCMV-SPORT6; Site-1: SalI; Site-2:
 NotI; This library represents the
 normalized version of
 NCI-CGAP-Ov23. Cloned
 unidirectionally. Primer: Oligo
 dT. Average insert size 0.86 kb.
 Tumor types include: mixed
 Mullerian tumor, papillary serous,
 clear cell, spindle cell. All are
 primary tumors, metastasis
 positive. Constructed by Life
 Technologies."

SEQUENCE (SEQ):

```

1 tttttttttt tttttttttt ttttttatgc atacacttct tggatttatt aatgctata
61 ttctatgaaa tccatgagta aatatagaaa cattgaaatt ccttctctct ctttagagtt
121 ttcttggtac gggatagtca gagtaacccc aaaactttcg tactgtcaat gagtcatgga
181 caaaaaataa agcacttca aattatacca gtaagtaatt cgtgatttca catttgtgta
241 ttagaaatga ccttaatgct aagctttga tcttaatgca taagctttg gaaactttgg
301 tttcttttg gncttttat taaatataat ttggcagctt gtgctttgac tagagccccg
361 cgtccgccc
  
```

L6 ANSWER 122 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI522272 GenBank (R)
 GenBank ACC. NO. (GBN): AI522272
 GenBank VERSION (VER): AI522272.1 GI:4436407
 CAS REGISTRY NO. (RN): 228602-27-5
 SEQUENCE LENGTH (SQL): 604
 MOLECULE TYPE (CI): mRNA; Linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 13 Apr 1999
 DEFINITION (DEF): ti84g01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
 IMAGE:2138736 3' similar to TR:Q14449 Q14449
 GRB14 . ;, mRNA sequence.
 SOURCE: human.
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo
 NUCLEIC ACID COUNT (NA): 160 a 118 c 118 g 208 t
 COMMENT:
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 1380 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 308.
 REFERENCE: 1 (bases 1 to 604)
 AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
 Project (CGAP), Tumor Gene Index
 JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..604	<code>/organism="Homo sapiens"</code> <code>/db-xref="taxon:9606"</code> <code>/clone="IMAGE:2138736"</code> <code>/clone-lib="NCI-CGAP-Kid11"</code> <code>/lab-host="DH10B"</code> <code>/note="Organ: kidney; Vector:</code>

pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP-Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "

SEQUENCE (SEQ):

```

1 ttcctaagg ttaatttaa ctaatgaatt ttaaatgatg aatgtaaagt caatccaagt
61 cttgcttat ttgcaatgca caaactattt tttgttaact tgccaggtaaa atacattctt
121 ttcacatgat aatgtttcg cccttattta tggtctttt ttatTTTCT tgagtccctt
181 tccttcaata gtttaataag tcacttctgg cttgtctaga gagcaatcct agcacaataa
241 tgtttcaact tgcaaggaaag aacgcctta ttgagttgat agaaactccac cagctgtatt
301 agatctgtaa atcttgcgtg gccatcatcc agtgtgtgaa acatTTcacc gtcatcttct
361 actggatataa ttgttgcgtg ctttattttt tggccatgac tcattgacag tacgaaagtt
421 ttgggggtac tctgactatc ccgtaccaag aaaactccat ccacaagtcc ttgctgaata
481 atcaatcgct gaggcctatc tcttagaaatt ttgtgtgaa accatggctg ggaccgggtgg
541 atagccatgt ttgtggcaaa gcttctggaa gaggcagggg ggctccggga gtgcccagggc
601 gtaa

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L6 ANSWER 123 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI505286 GenBank (R)
 GenBank ACC. NO. (GBN): AI505286
 GenBank VERSION (VER): AI505286.1 GI:4403137
 CAS REGISTRY NO. (RN): 228210-72-8
 SEQUENCE LENGTH (SQL): 578
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 11 Mar 1999
 DEFINITION (DEF): vp98h08.x1 Stratagene mouse diaphragm (#937303) Mus musculus cDNA clone IMAGE:1092831 3' similar to TR:Q14449 Q14449 ***GRB14*** . ;, mRNA sequence.
 SOURCE: house mouse.
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus
 NUCLEIC ACID COUNT (NA): 148 a 135 c 111 g 179 t 5 others
 COMMENT:

Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:599063

This clone was previously sequenced on the 5' end only, this new data is from the 3' end

High quality sequence stop: 379.

REFERENCE: 1 (bases 1 to 578)
 AUTHOR (AU): Marra,M.; Hillier,L.; Kucaba,T.; Martin,J.; Beck,C.; Wylie,T.; Underwood,K.; Steptoe,M.; Theising,B.; Allen,M.; Bowers,Y.; Person,B.; Swaller,T.; Gibbons,M.; Pape,D.; Harvey,N.; Schurk,R.; Ritter,E.; Kohn,S.; Shin,T.; Jackson,Y.; Cardenas,M.; McCann,R.; Waterston,R.; Wilson,R.
 TITLE (TI): The WashU-NCI Mouse EST Project 1999
 JOURNAL (SO): Unpublished (1999)

FEATURES (FEAT):

Feature Key	Location	Qualifier
-------------	----------	-----------

source 1..578 /organism="Mus musculus"
 /db-xref="taxon:10090"
 /clone="IMAGE:1092831"
 /clone-lib="Stratagene mouse
 diaphragm (#937303)"
 /tissue-type="diaphragm"
 /dev-stage="adult"
 /lab-host="SOLR (kanamycin
 resistant)"
 /note="Organ: diaphragm; Vector:
 pBluescript SK-; Site-1: EcoRI;
 Site-2: XhoI; Cloned
 unidirectionally from mRNA
 prepared from diaphragm muscle.
 Primer: oligo dT. Average insert
 size: 1.5 kb. Uni-ZAP XR Vector;
 ~5' adaptor sequence: 5'
 GAATTGGCACGAG 3' ~3' adaptor
 sequence: 5'
 CTCGAGTTTTTTTTTTTTTTTTTT

SEQUENCE (SEQ):

1 aataagggtt aatttttaact aataaaattta aaggcatgag tgtaatagga atccaagttt
 61 tcactaattt gcaatgtgtg acctattttt tttttaacc cgcagggtgaa atcttctttt
 121 caccatgggtt tgttttcagc cttgtatct ctctctctt ctctaatcat tctcctttgc
 181 atccttcttc ttctgttagtga taacgagtga cacacagttt ggctaaacag ccatccttagc
 241 acagtaatgc tttagtgc aaggaggac cccctgttg agctggtaga actccaccag
 301 ctggatgagg tctgtgaaact tcgtatggcc atcatccaga gtagtggaaaca gctcaccatc
 361 atcttctacg ggtataatnt gatagtgtt tatctttgtt ccatgactca ttgacagttac
 421 aaaagtctg gggttactct gactatcccg taccaagaaa actncatcca caggcccctg
 481 cccaaatgatc agncgtgag cctcatctt taaaatnctg tggtaaaacc catgttggac
 541 cgatggaaac catgttca cccanaactctt ggaaggcc

L6 ANSWER 124 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI494168 GenBank (R)
 GenBank ACC. NO. (GBN): AI494168
 GenBank VERSION (VER): AI494168.1 GI:4395171
 CAS REGISTRY NO. (RN): 228132-01-2
 SEQUENCE LENGTH (SQL): 368
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 13 Apr 1999
 DEFINITION (DEF): ti14f01.y1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
 IMAGE:2130457 5' similar to TR:Q14449 Q14449
 GRB14 . ;, mRNA sequence.

SOURCE: human.
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo

NUCLEIC ACID COUNT (NA): 98 a 71 c 58 g 141 t

COMMENT:

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 416 Std Error: 0.00
 Seq primer: -40RP from Gibco.

REFERENCE: 1 (bases 1 to 368)
 AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
 Project (CGAP), Tumor Gene Index
 JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..368	/organism="Homo sapiens" /db-xref="taxon:9606"

/clone="IMAGE:2130457"
 /clone-lib="NCI-CGAP-Kid11"
 /lab-host="DH10B"
 /note="Organ: kidney; Vector:
 pT7T3D-Pac (Pharmacia) with a
 modified polylinker; Site-1: Not
 I; Site-2: Eco RI; Plasmid DNA
 from the normalized library
 NCI-CGAP-Kid3 was prepared, and ss
 circles were made in vitro.
 Following HAP purification, this
 DNA was used as tracer in a
 subtractive hybridization
 reaction. The driver was
 PCR-amplified cDNAs from a pool of
 5,000 clones made from the same
 library (cloneIDs 1322376-1323911,
 1456007-1456775, and
 1500552-1502855). Subtraction by
 Bento Soares and M. Fatima
 Bonaldo. "

SEQUENCE (SEQ):

```

1 tcctaagggtt taattttaac taatgaattt taaatgatga atgtaaaagtc aatccaagtc
61 tttgcttatt tgcaatgcac aaactathtt tttgttaactt gcaggtgaaa tacattcttt
121 tcacatgata atgttttcgc ctttattttat ggtcttttat tattttctt gagtcccttt
181 ccttcaatag tttataaagt cacttctggc ttgtcttagag agcaatcccta gcacaataat
241 gtttcaactt gcaaggaaaga acgcccttat tgagttgata gaactccacc agctgtattt
301 gatctgtaaa tcttgtgtgg ccatcatcca gtgtgtggaa catttcaccgc tcattttctc
361 ctcgtgcc
  
```

L6 ANSWER 125 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI425417 GenBank (R)
 GenBank ACC. NO. (GBN): AI425417
 GenBank VERSION (VER): AI425417.1 GI:4271348
 CAS REGISTRY NO. (RN): 226504-01-4
 SEQUENCE LENGTH (SQL): 503
 MOLECULE TYPE (CI): mRNA; Linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 15 Mar 2000
 DEFINITION (DEF): my18a09.y1 Barstead mouse heart MPLRB3 Mus musculus
 cDNA clone IMAGE:696184 5' similar to TR:Q14449 Q14449
 GRB14 . ;, mRNA sequence.

SOURCE: house mouse.
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 103 a 171 c 143 g 86 t

COMMENT:

Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

This read is a RESEQUENCE of a previously sequenced mouse clone

This read has been verified (found to hit its original self in the
 correct orientation)

MGI:429744

Seq primer: -40RP from Gibco

High quality sequence stop: 493

POLYA>No.

REFERENCE: 1 (bases 1 to 503)

AUTHOR (AU): Marra,M.; Hillier,L.; Kucaba,T.; Martin,J.; Beck,C.;
 Wylie,T.; Underwood,K.; Steptoe,M.; Theising,B.;
 Allen,M.; Bowers,Y.; Person,B.; Swaller,T.;
 Gibbons,M.; Pape,D.; Harvey,N.; Schurk,R.; Ritter,E.;
 Kohn,S.; Shin,T.; Jackson,Y.; Cardenas,M.; McCann,R.;
 Waterston,R.; Wilson,R.

TITLE (TI): The WashU-NCI Mouse EST Project 1999

JOURNAL (SO): Unpublished (1999)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..503	/organism="Mus musculus" /strain="BALB/c" /db-xref="taxon:10090" /clone="IMAGE:696184" /clone-lib="Barstead mouse heart MPLRB3" /sex="mixed" /tissue-type="heart" /dev-stage="6 weeks" /lab-host="DH10B" /note="Organ: heart; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: EcoRI; Site-2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACGAATCTGAAGTGGGAGCGGCCGCCCTT TTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors [CTTGGATTCTGGTACC], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead."

SEQUENCE (SEQ):

1 aattcggatc caaggcaagg cgctcgctgc ctgcaaccgc tcggctctgc tcgccccag
61 cccttcgtag ctttcgcctc ggggtcgatg actccctaga cccctggccct acgaccatga
121 ccacgtccct gcaagacggg cagagcggc cgggccggc aggcgcggc gattcgccgc
181 tggcagtgcgca ggtgtgccgc gttgcccagg gcaaggaga cgcccaggac cggcgcagg
241 tccccggact gcacgcgctg tccccggctt ccgatgcgac cttccgcggt gccatagaca
301 ggagaaaaat gaaagatctg gatgttctgg aaaagccacc cattcccaac cccttcctg
361 agctctgctg ctctccgctt acatctgtgc tgtcagcagg cctgtttccc agggccaatt
421 caaggaagaa gcaggtgatt aaagttaca gcgaggatga aaccagcaga gcattagagg
481 tgcccagtga catcacagcc cga

L6 ANSWER 126 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC):	AI383743	GenBank (R)
GenBank ACC. NO. (GBN):	AI383743	
GenBank VERSION (VER):	AI383743.1	GI:4196524
CAS REGISTRY NO. (RN):	225333-52-8	
SEQUENCE LENGTH (SQL):	423	
MOLECULE TYPE (CI):	mRNA; linear	
DIVISION CODE (CI):	Expressed sequence tag	
DATE (DATE):	18 Mar 1999	
DEFINITION (DEF):	tc47e05.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2067776 3' similar to TR:Q14449 Q14449 ***GRB14*** . ;, mRNA sequence.	
SOURCE:	human.	
ORGANISM (ORGN):	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo	

NUCLEIC ACID COUNT (NA): 116 a 74 c 69 g 162 t 2 others

COMMENT:

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 967 Std Error: 0.00
Seq primer: -40UP from Gibco.

REFERENCE:	1 (bases 1 to 423)
AUTHOR (AU):	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
TITLE (TI):	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL (SO):	Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..423	/organism="Homo sapiens"

/db-xref="taxon:9606"
 /clone="IMAGE:2067776"
 /clone-lib="Soares-total-fetus-Nb2
 HF8-9w"
 /dev-stage="8-9 weeks"
 /lab-host="DH10B"
 /note="Vector: pT7T3D-Pac
 (Pharmacia) with a modified
 polylinker; Site-1: Not I; site-2:
 Eco RI; 1st strand cDNA was
 prepared from mRNA obtained from
 pooled 8-9 week (total) fetus
 material with a Not I - oligo(dT)
 primer [5'
 TGTTACCAATCTGAAGTGGGAGCGGCCGCTTAAT
 TTTTTTTTTTTTTTT 3'].
 Double-stranded cDNA was ligated
 to Eco RI adaptors (Pharmacia),
 digested with Not I and cloned
 into the Not I and Eco RI sites of
 the modified pT7T3 vector. Library
 went through one round of
 normalization, and was constructed
 by Bento Soares and M. Fatima
 Bonaldo. "

SEQUENCE (SEQ):

1 ccttaaggttt aattttaact aatgaatttt aaatgatgaa tgtaaagtca atccaaagtct
 61 ttgcttattt gcaatgcaca aactatttt ttgttaacttg caggtgaaat acattctttt
 121 cacatgataa cgttttcgcc ctatattatg gtcttttattt atttttcttg agtccttttc
 181 cttcaatagt ttaataaagtc acttctggct tgcgttagaga gcaatcctag cacaataatg
 241 ttcaacttg caaggaagaa cggcccttattt gagttgatag aactccacca gctgtttag
 301 atctgttaat cttgtgtggc catcatccag tgcgttggaaat atttcaccgt catcttctac
 361 tggtataattt ngaaagtgc ttatntttt gtcatgactc attgacagta caaaagtttt
 421 ggg

L6 ANSWER 127 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI364971 GenBank (R)
 GenBank ACC. NO. (GBN): AI364971
 GenBank VERSION (VER): AI364971.1 GI:4124660
 CAS REGISTRY NO. (RN): 224494-55-7
 SEQUENCE LENGTH (SQL): 318
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 16 Feb 1999
 DEFINITION (DEF): qz41h03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
 IMAGE:2029493 3' similar to TR:Q14449 Q14449
 GRB14 . ;, mRNA sequence.
 SOURCE: human.
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo

NUCLEIC ACID COUNT (NA): 90 a 54 c 48 g 125 t 1 others

COMMENT:

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 447 Std Error: 0.00

Seq primer: -40UP from Gibco.

REFERENCE: 1 (bases 1 to 318)

AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE (TI): National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key

Location

Qualifier

SEQUENCE (SEQ):

1 ttccctaagggt ttaattttaa ctaatgaatt ttaaatgatg aatgtaaagt caatccaagt
61 ctttgcttat ttgcaatgca caaactattt ttttgttaact tgcaggtaaa atacattttt
121 ttcacatgat aatgtttcg cccttattta tggncattta ttatttttct tgagtccctt
181 tccttcaata gtttaataag tcacttctgg cttgtctaga gagcaatcc agcacaataaa
241 tgtttcaact tgcaaggaaag aacgcctta ttgagttgat agaactccac cagctgtatt
301 agatctgtaa atcttgg

L6 ANSWER 128 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI263214 GenBank (R)
GenBank ACC. NO. (GBN): AI263214
GenBank VERSION (VER): AI263214.1 GI:3871417
CAS REGISTRY NO. (RN): 221598-25-0
SEQUENCE LENGTH (SQL): 382
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 3 Feb 1999
DEFINITION (DEF): qz36f04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
IMAGE:2028991 3' similar to TR:Q14449 Q14449
GRB14 ; mRNA sequence.

SOURCE: human.
ORGANISM (ORGN): *Homo sapiens*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; *Homo*

NUCLEIC ACID COUNT (NA): 112 a 59 c 56 g 154 t 1 others

COMMENT:

Contact: Robert Strausberg, Ph.D.

Email: cqapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Issue Prevalence: 6.1%
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares Ph.D.

CDNA Library Preparation: M. Bento Soares,
CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, PH.D.
DNA Sequencing by: Washington University Genome Sequencing Center

DNA sequencing by: Washington University Genome
Clone distribution: NCT-CCAP clone distribution

clone distribution: NCI-CGAP clone distribution found through the T.M.A.G.E. Consortium

Produced through the I.M.A.G.E. Consortium/LLNL at:
www-bis.llnl.gov/bbrnp/image/image.html

www-bio.ihl.gov/bbrp/image/image.html
Insert Length: 730 Std Energy: 0.00

Insert Length: 730 Std Error: 0.00
Seq primary: 40HR from Sibbs

Seq primer: -400UP from Gibco
High quality sequence starts: 381

High quality sequence stop: 381.

RENCE: 1 (bases 1 to 382)
THER (111)

AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/CGAP>

TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key Location Qualifier

source 1..382 /organism="Homo sapiens"

/db-xref="taxon:9606"
 /clone="IMAGE:2028991"
 /clone-lib="NCI-CGAP-Kid11"
 /lab-host="DH10B"
 /note="Organ: kidney; Vector:
 pT7T3D-Pac (Pharmacia) with a
 modified polylinker; Site-1: Not
 I; Site-2: Eco RI; Plasmid DNA
 from the normalized library
 NCI-CGAP-Kid3 was prepared, and ss
 circles were made in vitro.
 Following HAP purification, this
 DNA was used as tracer in a
 subtractive hybridization
 reaction. The driver was
 PCR-amplified cDNAs from a pool of
 5,000 clones made from the same
 library (cloneIDs 1322376-1323911,
 1456007-1456775, and
 1500552-1502855). Subtraction by
 Bento Soares and M. Fatima
 Bonaldo. "

SEQUENCE (SEQ):

1 tttttttttt tttttttttt cctaaggttt aatttttaact aatgaatttt aatgtatgaa
 61 tgtaaaagtca atccaaagtct ttgcttattt gcaatgcaca aactattttt ttgttaacttg
 121 cagggaaat acattctttt cacatgataa tgtttgcctt cttatattatg gtcttttatt
 181 attttcttg agtcctttc cttcaatagt ttaataagtc acttctggct tgtctagaga
 241 gcaatcctag cacaataatg ttcaacttg caagaaaaaa cgcccttatt gagttgatag
 301 aactcacaca cacgccccctt tggggtttta attttttaaa aggaaaaatt tcccgggttgg
 361 gggtttnaa aaaaaaaaaaa aa

L6 ANSWER 129 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AF076619 GenBank (R)
 GenBank ACC. NO. (GBN): AF076619
 GenBank VERSION (VER): AF076619.1 GI:3650499
 CAS REGISTRY NO. (RN): 216295-93-1
 SEQUENCE LENGTH (SQL): 1950
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Rodents
 DATE (DATE): 26 Sep 1998
 DEFINITION (DEF): Rattus norvegicus molecular adapter rGrb14 (***Grb14***) mRNA, complete cds.
 SOURCE: Norway rat.
 ORGANISM (ORGN): Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Rattus
 NUCLEIC ACID COUNT (NA): 546 a 460 c 500 g 444 t
 REFERENCE:
 AUTHOR (AU): Kasus-Jacobi,A.; Perdereau,D.; Auzan,C.; Clauser,E.;
 van Obberghen,E.; Mauvais-Jarvis,F.; Girard,J.;
 Burnol,A.F.
 TITLE (TI): Identification of the rat adapter ***Grb14*** as an
 inhibitor of insulin actions
 JOURNAL (SO): J. Biol. Chem., 273 (40), 26026-26035 (1998)
 OTHER SOURCE (OS): CA 130:20710
 REFERENCE:
 AUTHOR (AU): Kasus-Jacobi,A.; Perdereau,D.; Burnol,A.-F.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (03-JUL-1998) UPR 1524, CNRS, 9 rue Jules
 Hetzel, Meudon 92190, France

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1950	/organism="Rattus norvegicus" /strain="Wistar" /db-xref="taxon:10116"
gene	1..1950	/gene="Grb14"
CDS	70..1686	/gene="Grb14" /note="signal transduction protein; Grb7 family member; binds the insulin receptor" /codon-start=1

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/product="molecular adapter
rGrb14"
/protein-id="AAC61478.1"
/db-xref="GI:3650500"
/translation="MTTSLQDGQSAAGRAGAQDS
PLAVQCRVAQGKGDQAQDPAQVPG
LHALSPASDATRRGAMDRRKAKDLEVQETPSIPN
PFPELCCSPLTSVLSAGLFPNS
RKKQVIKVSEDETSRALEVPSVTARDVCQLLI
LKNHYVDDNSWTLFEHLSHTGVER
TVEDHELLTEVLSHWVMEEDNKLYLRKNYAKYEF
FKNPAMYFFPEHMVSFATEMNGDRS
LTQIPQVFLSSNTYPEIHGFLHAKEQGKKSWKKA
YFFLRRSGLYFSTKGTSKERPLHQ
FFSEFSTSNVYMSLAGKKHGAPTPYGFCKPTK
AGGPRDLKMLCAEEDQSRMCWTA
IRLLKYGMQLYQNYMHPQSARASACSSQSVPQRS
VSENSLVAAMDMSGQKTRVIDNPTE
ALSVAVEEGLAWRKKGCLRLGNHGSPTAPSQSSA
VNMALHRSQPWFHHRISRDEAQQL
ITRQGPVDGVFLVRDSQSNSPRTFVLSMSHGQKIK
HFQIIPVEDDGEVFTLDDGHTKF
TDLIQLVEFYQLNKGVLPCKLHYCARMAV"

```

SEQUENCE (SEQ):

```

1 gctggacccc agcctttctt cgctttcgcc tcgcggtcga tgactcccta gacccctgg
61 cctacgatca tgaccacgtc cctgcaagat gggcagagcg ccgcggcccg ggcggggcgcc
121 caggactccc cgctggcagt gcagggtgtgc cgcgttgcgg aggcaaggag agacgcccag
181 gaccggcgtc aggtcccccgg actgcacgcg ctgtcccccgg cctcagatgc gacccggccgc
241 ggtgccatgg acaggagaaa agcggaaagat ctggaagttc agggaaacgc ttccattcct
301 aacccttcc ctgagctcg ctgttctcca cttacatcg tgctgtcagc aggcccttcc
361 cccagatcaa attcaaggaa gaaacaggtg attaaagttt acagcggaga tgagaccagc
421 agagcgttag aggtgcccag tgacgtcaca gcccgtgatg tctgcccagct gttgatcctg
481 aagaaccact atgtcgacga caatagctgg acccttttg agcaccgtc tcacacaggc
541 gtagaaagga cagtggagga ccatagctg ctgactgaag tgcgtgtctca ttgggtgatg
601 gaagaagata ataagctgta tcttagaaag aattatgcca aatatgaatt ttttaagaac
661 ccaatgtatt tctttccaga gcacatggtg tctttgcaaa ctgaaatgaa cggtgacaga
721 tcccttacac agatcccgca ggtgtttta agctcaaaca catatcctga aatccatggc
781 ttcctgcatg caaaggaaca ggggaagaag tcttggaaaa aagcttactt ttttctcaga
841 agatctggtt tatattttc tactaaaggc acatccaagg aaccacggca cttgcagtt
901 ttcagtgaat tcagcactag taatgtttac atgtcactgg caggcaaaaa aaagcatgga
961 gcgccgactc cctatggatt ctgctttaag cctaccaaag caggaggccc cgggacactg
1021 aaaatgtgt gtgcagaaga agaccaaagc aggatgtgct ggtgaccgc cattagattg
1081 ctcagaatgt gcatgcagct ctaccagaat tatatgcattt catcccaagc tagaagcgcc
1141 tgcagtctc agagcgtatc accatgaga agcgtatcag agaattccct agtagcaatg
1201 gacttctcag gtcagaagac cagagtcatc gacaacccca ctgaagccct ttccgttgcc
1261 gttgaggaag gactcgctt gggggaaaaa ggtatgtttc gcctggggaa tcatgggagt
1321 cccactgcgc cctctcagag ctgtgtgt aacatggc tccacccggc ccagccatgg
1381 tttcaccaca gaattttagt agatgaagct cagcgttga ttacccggca ggggcctgtg
1441 gatggagttt tcttggtagc ggatagttagt agtaacccca gaatttttgt actgtcaatg
1501 agtcacggac aaaagataaa acactttcaa attatacccg tggaaagatga tggtgagggt
1561 ttccacaccc tggatgatgg ccatacgaag ttcacagatc tcatccagct cgtggagttc
1621 taccagctca acaagggggc ctttcttgc aagctgaagc attactgtgc taggatggct
1681 gtttagccaa actgtctgt actcgtaaa ctatggaaaga tggaggatgc aaagaagaat
1741 gattagagag agagagagag agagagagag agagagagag agagagagag agagaggaga
1801 tcacaaggct ggaaacaat catggtggaaa agaagattca cctgtgggtt acaaaaaaaat
1861 aggtcacgtt ttgcaaaattttaa gtgaagactt ggattcgat tactctcgat actttaaatt
1921 tattagttaa aattaaaccc tattaaaaaaa

```

L6 ANSWER 130 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI094433 GenBank (R)
 GenBank ACC. NO. (GBN): AI094433
 GenBank VERSION (VER): AI094433.1 GI:3433409
 CAS REGISTRY NO. (RN): 392191-42-3
 SEQUENCE LENGTH (SQL): 420
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 10 Nov 1998
 DEFINITION (DEF): ou87b07.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens
 cDNA clone IMAGE:1634773 3' similar to TR:Q14449 Q14449
 GRB14 . ;, mRNA sequence.
 SOURCE: human.
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;

Hominidae; Homo

NUCLEIC ACID COUNT (NA): 115 a 75 c 67 g 163 t

COMMENT:

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 796 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 277.

REFERENCE: 1 (bases 1 to 420)

AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE (TI): National Cancer Institute, Cancer Genome Anatomy

Project (CGAP), Tumor Gene Index

JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..420	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:1634773" /clone-lib="Soares-NSF-F8-9W-OT-PA -P-S1" /lab-host="DH10B" /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHSF pool 1: 309384-310919, 323208-325895 Soares Nb2HP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares Nb2HF8-9W pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 304776-306311, 320136-322823, 326280-326663 Soares NbHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."

SEQUENCE (SEQ):

1 cctaaggttt aatttttaact aatgaatttt aaatgatgaa tggtaaagtca atccaaagtct
61 ttgcttattt gcaatgcaca aactattttt ttgttaacttg caggtgaaat acattcttt
121 cacatgataa cgttttcgcc cttatttatg gtcttttattt atttttcttg agtccctttc
181 cttcaatagt ttaataaagtc acttctggct tgtcttagaga gcaatcctag cacaataatg
241 tttcaacttg caaggaagaa cggcccttattt gagttgatag aactccacca gctgtattag
301 atctgttaat ctttgttgcc catcatccag tgtgtgaaac atttcaccgt catcttctac
361 tggataatt tgaaagtgtct ttattttttgc tccatgactc attgacagta cgaaagtttt

L6 ANSWER 131 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AA917917 GenBank (R)

GenBank ACC. NO. (GBN): AA917917

GenBank VERSION (VER): AA917917.1 GI:3057807

CAS REGISTRY NO. (RN): 206814-02-0

SEQUENCE LENGTH (SQL): 497

MOLECULE TYPE (CT): mRNA; linear

DIVISION CODE (CI): Expressed sequence tag

DATE (DATE): 10 Jun 1998

DEFINITION (DEF): 0176g09.s1 NCI_CGAP_Kid3 Homo sapiens cDNA clone

IMAGE:1535584 3' similar to TR:Q14449 Q14449

GRB14 . ;, mRNA sequence.

SOURCE: human.
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 136 a 95 c 79 g 187 t

COMMENT:

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 664 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 440.

REFERENCE: 1 (bases 1 to 497)

AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index

JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature	Key	Location	Qualifier
source	1..497		/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:1535584" /clone-lib="NCI-CGAP-Kid3" /lab-host="DH10B" /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "

SEQUENCE (SEQ):

1 catttttttc ctaagggtta attttaacta atgaattttt aatgatgaat gtaaaagtcaa
61 tccaaagtctt tgcttatttg caatgcacaa actatttttt tctaacttgc aggtgaaata
121 catttttttc acatgataat gtttgcgcc ttatttatgg tcttttattta tttttcttga
181 gtccttttcc ttcaatagtt taataagtca cttctggctt gtctagagag caatccatgc
241 acaataatgt ttcaacttgc aaggaagaac gcccttattt agttgataga actccaccag
301 ctgtatttga tctgttaatc ttgtgtggcc atcatccagt gtgtggaaaca tttcaccgtc
361 atcttctact ggtataattt gaaagtgcctt tattttctgt ccatgactca ttgacagttac
421 gaaagttttt gggttactct gactatcccg taccaagaaa actcatccac aagtcccttgc
481 tgaataatca atcgctg

L6 ANSWER 132 OF 135 GENBANK.RTM. COPYRIGHT 2004 ON STN

LOCUS (LOC): AA684351 GenBank (R)

GenBank ACC. NO. (GBN): AA684351

GenBank VERSION (VER): AA684351.1 GI:2670937

CAS REGISTRY NO. (RN): 200792-61-6

SEQUENCE LENGTH (SQL): 503

MOLECULE TYPE (CI): mRNA; linear

DIVISION CODE (CI): Expressed sequence tag

DATE (DATE): 9 Dec 1997

DEFINITION (DEF): vm69d04.s1 Knowles Solter mouse 2 cell Mus musculus
cDNA clone IMAGE:1003495 5' similar to TR:Q14449 Q14449

GRB14 . ;, mRNA sequence.

SOURCE: house mouse.

ORGANISM (ORGN): *Mus musculus*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; *Mus*

NUCLEIC ACID COUNT (NA): 127 a 121 c 135 g 120 t

COMMENT:

Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:567711

Possible reversed clone: similarity on wrong strand
High quality sequence stop: 459.

REFERENCE: 1 (bases 1 to 503)

AUTHOR (AU): Marra,M.; Hillier,L.; Allen,M.; Bowles,M.; Dietrich,N.;
Dubuque,T.; Geisel,S.; Kucaba,T.; Lacy,M.; Le,M.;
Martin,J.; Morris,M.; Schellenberg,K.; Steptoe,M.;
Tan,F.; Underwood,K.; Moore,B.; Theising,B.; Wylie,T.;
Lennon,G.; Soares,B.; Wilson,R.; Waterston,R.

TITLE (TI): The WashU-HHMI Mouse EST Project

JOURNAL (SO): Unpublished (1996)

FEATURES (FEAT):

Feature	Key	Location	Qualifier
source	1..503		/organism="Mus musculus" /strain="B6D2 F1/J" /db-xref="taxon:10090" /clone="IMAGE:1003495" /clone-lib="Knowles Solter mouse 2 cell" /tissue-type="embryo" /dev-stage="2-cell" /lab-host="DH10B" /note="Organ: embryo; Vector: pBluescribe (modified); Site-1: MluI; Site-2: SalI; Cloned unidirectionally from mRNA prepared from 13,500 2-cell stage embryos. Primer: SalI(dT): 5'-CGGTCGACCGTCGACCGTTTTTTTTTTTT T-3'. DNAs were cloned into the MluI/SalI sites of a modified pBluescribe vector using commercial linkers (NEB). Average insert size: 1.2 kb."

SEQUENCE (SEQ):

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481 ctgtgcttagg atggctttt agc

L6 ANSWER 133 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): HSU69276 GenBank (R)

GenBank ACC. NO. (GBN): U69276

GenBank VERSION (VER): U69276.1 GI:1546834

CAS REGISTRY NO. (RN): 181109-72-8

SEQUENCE LENGTH (SQL): 2504

MOLECULE TYPE (CT): mRNA; linear

DIVISION CODE (CI): Primates

DATE (DATE): 17 Sep 1996

DEFINITION (DEF): Human hGrb1Rbeta/hGrb10 (GRB1Rbeta/GRB10) mRNA,
complete cds.

SOURCE: human.

ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo
 NUCLEIC ACID COUNT (NA): 639 a 652 c 654 g 555 t 4 others
 REFERENCE:
 AUTHOR (AU): Frantz,J.D.; Giorgetti-Peraldi,S.; Ottinger,E.A.;
 Shoelson,S.E.
 TITLE (TI): Human Grb1Rbeta/Grb10: Splice Variants of an Insulin
 and Growth Factor Receptor-Binding Protein with PH and
 SH2 Domains
 JOURNAL (SO): Unpublished
 REFERENCE:
 AUTHOR (AU): Frantz,J.D.; Giorgetti-Peraldi,S.; Ottinger,E.A.;
 Shoelson,S.E.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (04-SEP-1996) Research Division, Joslin
 Diabetes Center, One Joslin Place, Boston, MA 02215,
 USA

FEATURES (FEAT):		Location	Qualifier
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source	1..2504		/organism="Homo sapiens" /db-xref="taxon:9606" /tissue-type="cerebellum and skeletal muscle"
gene CDS	1..2504 288..1898		/gene="GRBIRbeta/GRB10" /gene="GRBIRbeta/GRB10" /note="signal transduction protein containing PH and SH2 domains and a potential SH3 domain interaction site; insulin receptor binding protein, binds the insulins, PDGF, and EGF receptors; splice variant of hGrbIR; member of the Grb7/Grb10/Grb14 family" /codon-start=1 /product="hGrbIRbeta/hGrb10" /protein-id="AAB08431.1" /db-xref="GI:1546835" /translation="MNASLESLYSACSMQSDTVP LLQNGQHARSQPRASGPPRSIQPQ VSPRQRVQRSQPVHILAVRRLQEEDQQFRTSSLP AIPNPFPELCPGSPPVLTGSLP PSQAAAKQDVKVFSEDGTSKVVEILADMTARDLC QLLVYKSHCVDDNSWTLVEHHPHL GLERCLEDHELVVQVESTMASESKFLFRKNYAKY EFFKNPMNFFPEQMVTWCQQSNGS QTQLLQNFLNSSSCPEIQGFLHVKELGKKSWKKL YVCLRRSGLYCSTKGTSKERPHLQ LLADLEDSNIFSLIAGRKQYNAPTDHGLCIKPNK VRNETKELRLLCAEDEQRTCWMT AFRLLKYEMLLYQNYRIPQQRKALLSPFSTPVRS VSENSLVAMDMSGTGRVIENPAE AQSAALEEGHAWRKRSTRMNILGSQSPLHPSTLS TVIHTQHWFHGRFSREESHRIIK QQGLVDGLFLRDSQSNSPKAFVLTLCCHHQKIKNF QILPCEDDGQTFFSLDDGNTKFSD LIQLVDFYQLNKGVLPCPKLKHHCIRVAL"

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2461 cgggtngga ttcaagctccc aaatgacaaa cccagccctt cccca

L6 ANSWER 134 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): HUMGRB14R GenBank (R)
GenBank ACC. NO. (GBN): L76687
GenBank VERSION (VER): L76687.1 GI:1369836
CAS REGISTRY NO. (RN): 391791-70-1
SEQUENCE LENGTH (SQL): 2376
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Primates
DATE (DATE): 6 May 1998
DEFINITION (DEF): Homo sapiens ***Grb14*** mRNA, complete cds.
SOURCE: human.
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo
NUCLEIC ACID COUNT (NA): 631 a 652 c 583 g 510 t
REFERENCE:
AUTHOR (AU): Daly, R.J.; Sanderson, G.M.; Janes, P.W.; Sutherland, R.L.
TITLE (TI): Cloning and characterization of ***GRB14***, a
novel member of the GRB7 gene family
JOURNAL (SO): J. Biol. Chem., 271 (21), 12502-12510 (1996)
OTHER SOURCE (OS): CA 125:27254

FEATURES (FEAT):

Feature Key	Location	Qualifier
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1321	tctggtttat	attttctac	taaaggaaca	tcaaaagg	cgcggcattt	gcagttttc
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1501	atgctctgt	cagaagaaga	gcagagtagg	acgtgc	tgaccgcgat	tagattgtct
1561	aagtatggca	tgcagctgt	ccagaattat	atgc	atcaaggtag	aagtggctgc
1621	agtccacaga	gcatatcacc	tatgagaagt	atatc	attccctgg	agcaatggac
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1801	actgcctt	caagagctc	tgccacaaac	atgg	accggtccca	gccatgg
1861	caccacaaa	tttctagaga	tgaggctcag	cgat	ttagcaagg	acttggat
1921	ggagtttct	ttgtacggg	tagtcagat	aaaa	tttctgtact	gtcaatggat
1981	catggacaaa	aaataaagca	cttcaatt	atacc	aagatgcgg	tgaatgttc
2041	cacacactgg	atgatggca	cacaagatt	acagatctaa	tacagctgtt	ggagttctat
2101	caactcaata	agggcgttct	tccttgc	ttgaaacatt	attgtgct	gattgctc
2161	tagacaagcc	agaagtact	tattaaacta	ttgaaaggaaa	aggactcaag	aaaaataata
2221	aaagaccata	aataagggcg	aaaacattat	catgtaaaa	aatgtat	cacctgc
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2341	tcatttaaaa	ttcatttagtt	aaaattaaac	ctttagg		

L6 ANSWER 135 OF 135 CONFSCI COPYRIGHT 2004 CSA on STN
AN 1999:27349 CONFSCI

DN 99-039843

TI Novel FGF signaling pathway u ***Grb14*** binds to FGF receptor 1
AU Reilly, J.F.; Mickey, G.; Maher, P.A.
CS Dep. Cell Biol., Scripps Res. Inst., La Jolla, CA 92037, USA
SO American Society for Cell Biology, 9650 Rockville Pike, Bethesda, MD
20814, USA; phone: (301) 530-7153; fax: (301) 530-7139; email:
ascbinfo@ascb.org; URL: www.ascb.org/ascb/, Abstracts available. Price
\$45. Paper No. 1365.

Meeting Info.: 984 0478: 38th American Society for Cell Biology Annual Meeting (9840478). San Francisco, CA (USA). 12-16 Dec 1998. ASCB, Bio-Rad, Genentech, Jeol USA, Johnson & Johnson, Leica, Leadership Alliance, Mark-Rambar Family Foundation.

DT Mark Rambo
FS Conference
DCCP

LA English

STN INTERNATIONAL LOGOFF AT 15:35:54 ON 05 JAN 2004